GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 4, 2002, 16:13:00 ; Search time 101.54 Seconds
(without alignments)
208.190 Million cell updates/sec

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Title: US-09-052-089A-4
Perfect score: 1075
Sequence: 1 KTIINKLFPDLAQEENVLD.........DLQSADQEITSLRKKSDDPP 220

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	Match ID	Description
1	522	48.6	433	2	T30807	TRAF interacting p
2	180	16.7	2139	2	T18296	myosin heavy chain
3	175.5	16.3	1827	2	T16270	hypothetical prote
4	175	16.3	1017	2	PC4035	cell-cycle-depende
5	169.5	15.8	1957	2	T38077	hypothetical colle
6	169	15.7	1938	2	JC5421	smooth muscle myos
7	168.5	15.7	1325	2	T42722	male-enhanced anti
8	168	15.6	484	2	B33501	myosin heavy chain
9	167.5	15.6	1203	2	B55094	chromosomal protei
10	166	15.4	2017	2	A36014	myosin heavy chain
11	166	15.4	2057	2	S61477	myosin II heavy ch
12	164.5	15.3	746	2	T47237	myosin II heavy ch
13	163	15.2	1313	2	F96673	hypothetical prote
14	163	15.2	1790	2	S67593	transport protein
15	162.5	15.1	2116	2	A26655	myosin heavy chain
16	162	15.1	1938	1	A40997	myosin heavy chain
17	161	15.0	296	2	I52860	smooth muscle myos
18	160.5	14.9	1744	2	JH0720	tanabin - African
19	160.5	14.9	1957	2	A59294	skeletal myosin -
20	160.5	14.9	1963	1	MKKW	myosin heavy chain
21	160	14.9	1972	1	JC5420	smooth muscle myos
22	159	14.8	963	1	A41919	smooth muscle myos
23	159	14.8	1972	1	A41604	kinesin heavy chai
24	158.5	14.7	1999	1	S21801	myosin heavy chain
25	157.5	14.7	886	2	H69378	myosin heavy chain
26	157	14.6	881	2	I84737	conserved hypothet
27	157	14.6	924	2	S06117	kinesin heavy chai
28	157	14.6	1738	2	T18867	myosin heavy chain
29	157	14.6	2007	1	B43402	interaptin - slime
30	156.5	14.6	1509	1	A27224	myosin heavy chain
31	156	14.5	412	2	S07537	myosin heavy chain
32	155	14.4	484	2	S60943	RUD3 protein - yea
33	155	14.4	1156	2	B70356	chromosome assembl
34	155	14.4	1690	2	T13030	microtubule bindin
35	154.5	14.4	380	2	T25454	hypothetical prote
36	154.5	14.4	1133	2	T22976	hypothetical prote
37	154.5	14.4	1201	2	C35815	myosin heavy chain
38	154.5	14.4	1175	2	D35815	myosin heavy chain
39	154.5	14.4	1175	2	A35815	myosin heavy chain
40	154.5	14.4	1201	2	B35815	myosin heavy chain
41	154.5	14.4	2385	2	A32491	myosin heavy chain
42	154.5	14.4	2411	2	B32491	myosin heavy chain
43	154	14.3	896	2	S43074	epidermal growth f
44	154	14.3	1976	2	A59252	epidermal growth f
45	153.5	14.3	1938	1	MKKW1	myosin heavy chain

ALIGNMENTS

RESULT 1
T30807
TRAF interacting protein - Fugu rubripes
C;Species: Fugu rubripes
C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000
C;Accession: T30807
R;Cottage, A.J.; Clark, M.; Hawker, K.; Umrania, Y.; Wheller, D.; Bishop, M.; Elgar,
FEBS Lett. 443, 370-374, 1999
A;Title: Three receptor genes for plasminogen related growth factors in the genome of
A;Reference number: Z20880; MUID:99148833
A;Accession: T30807
A;Molecule type: DNA
A;Residues: 1-433 <COT>
A;Cross-references: EMBL:AJ010317; NID:e1355235; PID:e1355237; PIDN:CAA09084.1
C;Genetics:
A;Gene: TRIP
A;Introns: 33/2; 52/3; 80/3; 94/1; 136/3; 168/2; 206/2; 235/3; 265/3; 310/1; 352/3; 3

Query Match   48.6%; Score 522; DB 2; Length 433;
Best Local Similarity 46.0%; Pred. No. 3.8e-22;
Matches   98; Conservative 59; Mismatches 56; Indels   0; Gaps   0;

Qy   3 INKLFPDLAQEENVLDAEFLKNELDSVKAQLSQKDREKRDSQAIIDTLRDTLEERNAT 62
            :::||:|||:||.::: :||||:::|:|:|||||||||:||:::::::|::|::::|
Db   58 IISRLYFDVGLDDSSVGDPESLQNELDRVKVNFSSKERDWREKQKAMDDLMETVELQRKA 117

Qy   63 VESLQNALNKAEMLCCSTLKKQMKFLEQRQDETKQAREEAHRLKCKMKTMEQIELLLQSQR 122
          :::||| ||::::||||:|.::||::::|:| |:||||:|| :::|||:||||||:||:||||
Db 118 LENLQKDVMEKELCSALRTQMTYLESQHDTRAAKEEVRRLRIKMKTFESLDVVLQGQR 177

Qy 123 SEVEEMIRDMGVGQSAVEQLAYVCVSLKKEYENLKEARKATGELADRLKIKDLVSSRSKLK 182
           :||| :::|:::|| ::::|||.| |:||:||:||||:|:::|||:||||||||::|:::|| ||
Db 178 AEVESMITDMGIGQAAVEQLSIYCISLKKEYDNLKGGLKSSNEMCEKLKREVLTSNNKLH 237

Qy 183 TLNTELDQAKLELRSAQKDLQSADQEITSLRKK 215
          ||::||||||::|||||||||||||||||||||||
Db 238 KALLELTKARDDMKSLQNDLTNAEKELSSLKKK 270

RESULT 2
T18296
myosin heavy chain - Entamoeba histolytica
C;Species: Entamoeba histolytica
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 08-Sep-2000
R;Guillen, N.
submitted to the EMBL Data Library, February 1997
C;Accession: T18296
A;Reference number: Z18865
A;Accession: T18296
A;Status: preliminary; translated from GB/EMBL/DDBJ

```
A:Molecule type: DNA
A:Residues: 1-2139 <GUI>
A:Cross-references: EMBL:L03534; NID:g1850912; PID:g1850913; PIDN:AAB48065.1
C:Genetics:
A:Gene: mhcA
C:Superfamily: myosin heavy chain; myosin motor domain homology
F:91-780/Domain: myosin motor domain homology <MMO>

Query Match      Best Local Similarity     27.6%;   Score 180;   DB 2;   Length 2139;
Matches    60;   Conservative   52;   Pred. No. 0.016;   Mismatches   77;   Indels   28;   Gaps   7;

Qy     11 LAQEENVLDAEFLKNELDSVKAQLSQK----------DREKRDSQAIIDTLRDTLEERNATV 63
             ::::::  ||:|: ||| :| :|: :|          : |::  |:||::  ::  : : :
Db   1671 VAQEEEK----QRLESDIAELKEQLEQERTTAANAEAERKIQAELDEVKFNLEDVTNQR 1726

Qy     64 ESL--QNALNKAEMLCSTLKQMKFLEQRQDETKQAREEAHRLCKCMKMTMEQIELLLQSQ 121
             |:|   |:|:|:    ||: ||  :| |:|:: |:|:     |:|: :  |||: :|
Db   1727 EKIVAKNSENDAEI--DSLKEEKRALE---DEIEKITDDNNKLS------EEIDSLDRKY 1775

Qy    122 RSEVEEMIRDMGVGQGSAVEQLAVYCVSLKKEYENLKEARKATGELADRLKKDLVSSRSKL 181
             |::: |:  |: |  :||::|  |   ||: |:|||:||:||:: ||  |::|::::|:|
Db   1776 NALLDSKDSDVSMKEKFQDELKVTKDALETEKKNHAETMRLKG----RLEKEAAEVQVRL 1831

Qy    182 KTLNTELDQAKLELRSAQKDLQSADQEITSLRKKSSD 218
             ::|:  |:  |  |  :|::| |:|:|::|::||: |
Db   1832 EALQKNLDLAQQEAKAATKDYRAADGELKSLMNELDD 1868

RESULT 3
T16270
hypothetical protein F35D11.11 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T16270
R:Fulton, B.
R:submitted to the EMBL Data Library, June 1995
A:Description: The sequence of C. elegans cosmid F35D11.
A:Reference number: 218487
A:Accession: T16270
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-1827 <FUL>
A:Cross-references: EMBL:U29381; NID:g868214; PID:g868224; PIDN:AAA68757.1; CESP:F35D11.
C:Genetics:
A:Experimental source: strain Bristol N2
A:Gene: CESP:F35D11.11
C:Genetics:
A:Introns: 76/2; 131/3; 159/3; 185/3; 221/3; 253/3; 320/1; 869/3; 1133/3; 1205/2; 1250/1

Query Match      Best Local Similarity     25.3%;   Score 175.5;   DB 2;   Length 1827;
Matches    58;   Conservative   61;   Pred. No. 0.024;   Mismatches   79;   Indels   31;   Gaps   8;

Qy      5 NKLFFDLAQEENVLD-----------AEFLKNELDSVKAQLSQKDREKRDSQAIIDTLR--- 53
Db    669 NEKYDDAARNDALLEDVATWQEKYEQLKMELEEMNRRGQEKEREEADLRALLDDLRGNF 728

Qy     54 ---DTLEERNATVESLQNALNKAEMLCSTLKKQM-KFLEQRQDETKQAREEAHRLCKCM 108
Db    729 DKLTNELKQKGVTVDSLNEEI-------SSLKEQLNKSEKERKEELLRMELEEQKNEAM 781

Qy    109 KTMEQIEL-LLQSQRSEVEEMIRDMGVGQGSAVEQLAVYCVSLKKEYENLKEARKATGELA 167
Db    782 KEEYEVKLQLAEKDRQGVENFGKEC---EARMELTKIHEMLMEEHDQLKVDHLHTEEEV 838

Qy    168 DRLKKDLVSSRSKLKTLNTELDQAKLELRSAQKDLQSADQE-ITSLRKK 215
Db    839 ERLKEKM---RKELEKLNEQNDGDRAEWSNERNRLESSKNEAVTELQER 884

RESULT 4
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```
PC4035
cell-cycle-dependent 350k nuclear protein - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 08-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 21-Jul-2000
C:Accession: PC4035
A:Note: repeat 15-160 and 200-340
C:Comment: This protein contains a coiled-coil and a globular domain at the carboxy-t
C:Cross-references: GB:U25725; NID:g818866; PIDN:AAA86889.1; PID:g818867
C:Keywords: nucleoprotein; phosphoprotein
F:465/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase II) #s
F:825,826,838/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #st
F:908,909/Binding site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status
A:Reference number: PC4035
A:Accession: PC4035
A:Molecule type: DNA
A:Residues: 1-1017 <LIQ>
A:Title: A novel cell-cycle-dependent 350-kDa nuclear protein: C-terminal domain suff
R:Li, Q.; Ke, Y.; Kapp, J.A.; Fertig, N.; Medsger Jr., T.A.; Joshi, H.C.
Biochem. Biophys. Res. Commun. 212, 220-228, 1995
F:825,826,838/Binding site: PC4035; MUID:95336446

Query Match      Best Local Similarity     21.8%;   Score 175;   DB 2;   Length 1017;
Matches    62;   Conservative   54;   Pred. No. 0.014;   Mismatches   100;   Indels   68;   Gaps   5;

Qy      1 KTIINKLFFDLAQEEEN---VLDAEFLKNELDSVKAQLSQKDREKRDSQAIIDTLRDTL 56
Db     56 KDKVENLERELQMSEENQELVILDAENSKAEVETLKTQIEEMARSLKVFELDLVTLRSEK 115

Qy     57 EERNATVESLQNALNKAEMLCSTLKKQMKFLEQRQ---------------------- 91
Db    116 ENLTKQIEQEKQGLSELDKLLSSFKSQLEEKEQAETQIKEESKTAVEMLQNQLKELNEAV 175

Qy     92 -------DETKQAREEAHRLCKCMKMTMEQIELLLQSQRSE--- 124
Db    176 AALCGDQEIMKATEQSLDPPIEEEHQLRNSIEKLRARLEADEKKQLCVLQQLKESEHHAD 235

Qy    125 --------VEEMIRDMGVGQGSAVEQLAVYCVSLKKEYENLKEARKATGELADRLKKDLVSSRS 179
Db    236 LLKGRVENLERELEIARTNQEHAALEAENSKGEVETLKAKIEGMTQSLRGLELDVTIRS 295

Qy    180 KLKTLNTELDQ-----AKLEL--RSAQKDLQSADQEITSLRKKS 216
Db    296 EKEDLTNELQKEQERISELEIINSSFENILQEKEQEKVQMKEKS 339

RESULT 5
T38077
hypothetical coiled-coil protein - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T38077
R:Connor, R.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
R:submitted to the EMBL Data Library, April 1996
A:Reference number: 221767
A:Accession: T38077
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-1957 <CON>
A:Cross-references: EMBL:Z70690; PIDN:CAA94624.1; GSPDB:GN00066; SPDB:SPAC1F3.06c
A:Experimental source: strain 972h-; cosmid c1F3
C:Genetics:
A:Gene: SPDB:SPAC1F3.06c
A:Map position: 1

Query Match      Best Local Similarity     22.4%;   Score 169.5;   DB 2;   Length 1957;
Matches    54;   Conservative   54;   Pred. No. 0.055;   Mismatches   96;   Indels   37;   Gaps   4;

Qy     15 EENVLDAEFLKNELDSVKAQLSQKDREKRDSQAIIDTLRDTLEERNATVESLQNALNKAE 74
Db   1386 EDNQLATNKLKNQLDHLNQEIRLKEDVLKEKESLIISLEESLSNQROKESSLLDAKNELE 1445
```

RESULT 6
JC5421

Qy   75 -MLCSTLKKQMKFLEQRQ--------DETKQAREEAHRLKCKMKTMEQIELLLQSQRSEVE 126
          : :|: ||:|| ||:|| |:|| |: |:|:
Db 1446 HMLDDTSRKNSSLMEKIESINSSLDDKSFELASAVEKLGALQKLHSESLSLMENIKSQLQ 1505

Qy   127 EMIRDMGVGQSAVEQLAVYCVSLKKEYEN----------------LKEARKATG 164
          | |:|:| |:| | | | || | :| ||:|| |
Db 1506 EAKEKIQVDESTIQELDHEITASKNNYEGKLNDKDSIIRDLSENIEQLNNLAEEKSAVK 1565

Qy   165 ELADRLRKDLVSSRSKLKTL-------NTELDQAKLERSAQKDLQSADQEITSLRKSD 217
          |||||||||||||||||| | ||| | | || || | | :| :||
Db 1566 RLSTEKESEILQFNSRLADLEYHKSQVESELGRSKLKLASTTEELQLAENERLSLTTRML 1625

Qy   218 D 218
          |
Db 1626 D 1626

A;Title: Cloning and expression of murine smooth muscle myosin heavy chains.
C;Species: Mus musculus (house mouse)
C;Date: 10-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 02-feb-2001
C;Accession: JC5421
R;Hasegawa, K.; Arakawa, E.; Oda, S.; Matsuda, Y.
Biochem. Biophys. Res. Commun. 232, 313-316, 1997
A;Reference number: JC5420; MUID:97241282
A;Accession: JC5421
A;Molecule type: mRNA
A;Residues: 1-1938 <HAS>
A;Cross-references: DDBJ:D85924; NID:g1945079; PIDN:BAA19691.1; PID:g1945080
A;Experimental source: smooth muscle
C;Comment: This protein plays a role in smooth muscle cell contraction.
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Keywords: nucleotide binding; P-loop
F;88-771/Domain: myosin motor domain homology <MMOT>
F;178-185/Region: nucleotide-binding motif A (P-loop)

smooth muscle myosin heavy chain 2 - mouse

Query Match   15.7%; Score 169; DB 2; Length 1938;
Best Local Similarity   22.6%; Pred. No. 0.058;
Matches   57; Conservative   53; Mismatches   94; Indels   48; Gaps   7;

Qy   10 DLAQEENVLDAEFLKNELDSVKAQLSOK--------------------DREKRDSQAIIDTLRDTLEE 58
          | |:|| | || || || | | | | | :| | | | ||
Db 1688 DLMQLQEDLAAAERARKQADLEKEELAEELASSLSGRNLQDEKRRLEARIAQLEELEE 1747

Qy   59 RNATVESLQNALNKAEMLCSTLKKQMKFLEQRQDETKQAREEAHR----------------- 103
          | ||:||| ||:|||: ||:|||||
Db 1748 EQGNMEAMSDRVRKATLQABQLSNELATERSTAQKNESARQQLERQNKELRSKLQEVEGA 1807

Qy   104 LKCKMK--TMEQIELLLQSQRSEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKA 162
          | |:| |:|:|| ||| | ||:| |:| |:| | | | || | :|||||
Db 1808 VKARLKSTVAALEAKIAQLEEQVEQEAREK---QAATKSLKQKDKKLKEVLLQVEDERK- 1863

Qy   163 TGELADRLRKDLVSSRSKLKTLNTELDQAKLE------LRSAQKDLQSADQ------E 208
          ||||||||||||||||||||||||||||| | | || || | |
Db 1864 ---MAEQXEQAEKGNTKVKQLRKQLEEAAEESQCINANRRKLQRELEDATESNEAMGRE 1920

Qy   209 ITSLRKKSDDPP 220
          |:|| ||
Db 1921 VNALKSKLRGPP 1932

A;Title: Characterization of a mammalian smooth muscle myosin heavy chain cDNA clone
C;Species: Mus musculus (house mouse)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000
R;Kondo, M.; Sutou, S.
DNA Seq. 7, 71-82, 1997

RESULT 7
T42722
male-enhanced antigen-2 - mouse

A;Title: Cloning and molecular characterization of cDNA encoding a mouse male-enhance
A;Reference number: T42722
A;Accession: Z22242; MUID:97217683
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1325 <KON>
A;Cross-references: EMBL:D78270; NID:d1096175; PID:d1020389; PIDN:BAA19612.1
A;Experimental source: strain CD-1
C;Function:
C;Description: supposed to play some role for spermatogenesis
C;Keywords: leucine zipper

Query Match   15.7%; Score 168.5; DB 2; Length 1325;
Best Local Similarity   23.8%; Pred. No. 0.042;
Matches   69; Conservative   50; Mismatches   84; Indels   87; Gaps   12;

Qy   10 DLAQEENVLDA-EFLKNE-------LDSVKAQLSOKDREKR------DSQAIIDTLRD 54
          | |:| | | || | | || | | | | || | |
Db   590 ELQREADSREDAIHFLQNEKIVLEVALQSAKSDKEELDRGARRLEEDTEETSGLLEQLRQ 649

Qy   55 TLEERNATVESLQNALNKAEMLCSTLKKQM-----KFLEQ------RQDET-----KQ 96
          ||| | | || | || | | |||| |
Db   650 DLAVKSNQVEHLQQE------TATLRKQMQKVKEQFVQQKVMVEAYRRDATSKDQLINE 702

Qy   97 AREEAHRLKCKMKTMEQIELLLQSQRSEVE----EMIRDMGVGQSAVEQLAVYCVSLKKE 152
          ||:||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db   703 LKATKTKRLDSEMKELRQELIKLQGEKKTVEVEHSRLQKDMDMSLVHQQMAELEGHLQSVQKE 762

Qy   153 YEN------------LKEA----RKATGELADRLRKDLVSSRSKLKTLNTELDQA 191
          | | |||| || | |||||||||||||||||||||||||
Db   763 RDEMEIHLQSLKFDKEQMIALTEANETLKKQIEELQQEAKKAITEQKQKMKRLGSDLITSA 822

Qy   192 KLELRSAQKDLQSA-----------------------DQEITSLRKK----SDDP 219
          | ||| ||||| | | |:|| || ||||
Db   823 QKEMKIKHKAYENAVSILSRRLQEALASKEATDAELHNQLRAQSTGGSSDP 872

RESULT 8
B33501
myosin heavy chain 2, smooth muscle - rabbit (fragment)

A;Title: Identification of two types of smooth muscle myosin heavy chain isoforms by
A;Reference number: A33501; MUID:89255535
A;Accession: B33501
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-484 <NAG>
A;Cross-references: GB:J04833
R;Nagai, R.; Kuro-o, M.; Babij, P.; Periasamy, M.
J. Biol. Chem. 264, 9734-9737, 1989
A;Accession: B33501; A31368
A;Molecule type: mRNA
A;Residues: 1-484 <NA2>
A;Cross-references: GB:J03614; NID:g165517; PIDN:AAA31406.1; PID:g165518
R;Nagai, R.; Larson, D.M.; Periasamy, M.
Proc. Natl. Acad. Sci. U.S.A. 85, 1047-1051, 1988
A;Reference number: A31368; MUID:88124972
A;Accession: A31368
A;Molecule type: mRNA
A;Residues: 1-484 <NA2>
A;Cross-references: GB:J03614; NID:g165517
A;Superfamily: myosin heavy chain; myosin motor domain homology
C;Keywords: muscle; smooth muscle

Query Match   15.6%; Score 168; DB 2; Length 484;
Best Local Similarity   23.0%; Pred. No. 0.016;
Matches   58; Conservative   52; Mismatches   94; Indels   48; Gaps   7;

Qy   10 DLAQEENVLDAEFLKNELDSVKAQLSOK--------------------DREKRDSQAIIDTLRDTLEE 58
          | |:|| | || || || | | | | | :| | | | ||
Db   234 DLMQLQEDLAAAERARKQADLEKEELAEELASSLSGRNALQDEKRRLEARIAQLEELEE 293

Species: Oryctolagus cuniculus (domestic rabbit)
Date: 08-Dec-1989 #sequence_revision 08-Dec-1989 #text_change 13-Aug-1999
Accession: B33501; A31368

```
Qy    59  RNATVESLQNALNK-------AEMLCSTLKKQMKFLEQRQDETKQAREEAHRLKCKMKTME--  112
              ::::::: :::::       :::  ::::::::::::::::::: : :::  :: :::
Db   294  EQGNMEAMSDRVRKATQQAEQLSNELATERSTAQKNESARQQLERQNKELKSKLQEMEGA  353

Qy   113  ----------QIELLLQSQRSEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKA  162
                     ::  ::::::::::::::::::::::::::::::::::::::::::::  ::
Db   354  VKSKFKSTIRALEAKIAQLEEQVEQEAREK---QAAAKALKQRDKKLKEMLLQVEDERK-  409

Qy   163  TGELADRLKKDLVSSRSRSKLKTLNTELDQAKLE--------LRSAQKDLQSADQ------  208
                ::::::::::::::::::::::::::::::::         ::: :::: :::
Db   410  ---MAEQYKEQAEKQNAKYVKQLKRQLEEAEEESQRINANRRKLQRELDEATESNEAMGRE  466

Qy   209  ITSLRKKSDDPP  220
              :::: :::::
Db   467  VNALKSKLRGPP  478


RESULT  9
B55094
chromosomal protein XCAP-E - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 02-Jun-2000
C;Accession: B55094
R;Hirano, T.; Mitchison, T.J.
R;Cell 79, 449-458, 1994
A;Title: A heterodimeric coiled-coil protein required for mitotic chromosome condensation
A;Reference number: A55094; MUID:95042742
A;Accession: B55094
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1203 <HIR>
A;Cross-references: GB:U13674; NID:g563813; PIDN:AAA64680.1; PID:g563814
C;Superfamily: chromosome segregation protein SMC1
C;Keywords: chromosomal protein; DNA condensation; heterodimer

Query Match          15.6%;  Score 167.5; DB 2; Length 1203;
Best Local Similarity  24.6%;  Pred. No. 0.043;
Matches   51; Conservative   45; Mismatches   80; Indels   31; Gaps   5;

Qy    22  EFLKNELDSVKAQLSQKDREKRDSQAIIDTLRDTLEERNATVESLQNALNKAEMLCSTLK  81
              :: ::: : :  ::: : :::  :: :: ::::::::::::::::::::::: :::::
Db   721  EMKSEEAELLQTKLQQSSYHKQQEE--LDSLKQITEESEETLKNTKEVQKKAEEFKVLE  778

Qy    82  KQMKFLE-QRQDETKQARE------------EAHRLKCKMKIMEQIELLLQSQRSEVEEMIRD  131
              :::::: : :: :::: :          ::: : :: :: : : : :::: :: ::::
Db   779  HKMKNAEAEREELKEAQOKLDTAKKADASNKKMKEKQQEVDALVL----ELEELKRE  833

Qy   132  MGVGQSAVEQLAVYCVSLKKEYENLKEARKATGELADRLKKDLVSSRSRSKLKTLNTELDQA  191
              ::::::::::::::::::::::::: :::::::::::::::::::::::::::::::: ::
Db   834  Q----------TTYKQOIETVDEAMKAYQEQADSMASEVSKNKEAVKKAQDELAKQ  879

Qy   192  KLELRSAQKDLQSADQEITSLRKKSDD  218
              :::::: : :::: ::: :: ::::
Db   880  KEIIMGHDKEIKTKSSEAGKLRENNND  906


RESULT  10
A36014
myosin heavy chain, nonmuscle - fruit fly (Drosophila melanogaster)
N;Contains: myosin ATPase (EC 3.6.1.32)
C;Species: Drosophila melanogaster
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Jan-2001
C;Accession: A36014; B36014
R;Ketchum, A.S.; Stewart, C.T.; Stewart, M.; Kiehart, D.P.
Proc. Natl. Acad. Sci. U.S.A. 87, 6316-6320, 1990
A;Title: Complete sequence of the Drosophila nonmuscle myosin heavy-chain transcript: co
A;Reference number: A36014; MUID:90349606
A;Accession: A36014
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-2017 <KET>
A;Cross-references: GB:M35012
```

```
C;Genetics:
A;Gene: FlyBase:zip
A;Cross-references: FlyBase:FBgn0005634
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Keywords: actin binding; alternative splicing; ATP; coiled coil; hydrolase; methyla
F;1-2017/Product: myosin heavy chain, form I #status predicted <MA1>
F;46-2017/Product: myosin heavy chain, form II #status predicted <MA2>
F;135-815/Domain: myosin motor domain homology <MMOT>
F;225-232/Region: nucleotide-binding motif A (P-loop)
F;598-631/Region: actin binding #status predicted
F;705-727/Region: actin binding #status predicted
F;888-2017/Domain: coiled coil homology #status predicted <COI>
F;888-1328/Region: S2
F;1329-2017/Region: light meromyosin
F;176/Modified site: N6,N6,N6-trimethyllysine (Lys) #status predicted
F;231/Binding site: ATP (Lys) #status predicted
F;745,755/Active site: Cys #status predicted


RESULT  11
S61477
myosin II heavy chain, non-muscle - fruit fly (Drosophila melanogaster)
R;Mansfield, S.G.; Al-Shirawi, D.Y.; Ketchum, A.S.; Newbern, E.C.; Kiehart, D.P.
submitted to the EMBL Data Library, September 1995
A;Reference number: S65349
A;Accession: S65349
A;Molecule type: DNA
A;Residues: 1-1908, NL', 1911-2057 <MAN>
A;Cross-references: EMBL:U35816; NID:g1141789; PIDN:AAB09049.1; PID:g1572481
R;Mansfield, S.G.; Al-Shirawi, D.Y.; Ketchum, A.S.; Newbern, E.C.; Kiehart, D.P.
J. Mol. Biol. 255, 98-109, 1996
A;Title: Molecular organization and alternative splicing in zipper, the gene that enc
A;Reference number: S61477; MUID:96144835
A;Accession: S61477
A;Molecule type: DNA
A;Residues: 1-2057 <MAW>
A;Cross-references: FlyBase:FBgn0005634
A;Introns: 10/3; 90/3; 162/3; 215/1; 255/3; 263/3; 303/3; 334/3; 1248/1; 1349/3; 1526
A;Cross-references: EMBL:U35816
R;Mansfield, S.G.; Al-Shirawi, D.Y.; Ketchum, A.S.; Newbern, E.C.; Kiehart, D.P.
C;Species: Drosophila melanogaster
C;Date: 19-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 02-Feb-2001
C;Accession: S61477; S65349
C;Genetics:
A;Gene: zip
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Keywords: alternative splicing; ATP; nucleotide binding; P-loop
F;135-855/Domain: myosin motor domain homology <MMOT>
F;225-232/Region: nucleotide-binding motif A (P-loop)

Query Match          15.4%;  Score 166; DB 1; Length 2017;
Best Local Similarity  25.2%;  Pred. No. 0.089;
Matches   61; Conservative   47; Mismatches   96; Indels   38; Gaps   8;

Qy     1  KTIINKLFFDLAQEEENVLDAE--FLKNELDSVKAQLSQKDREKRDSQ----------AI  48
              ::::                :::::::::::::::::::::::          ::
Db  1263  KTVLEK--------AKGTLEAENADLATELRSVNSSRQENDRRKQAESQIAELQVKLAE  1314

Qy    49  IDTLRDTLEER----NATVESLQNALNKAEMLCSTLKKQMKFLEQRQDETKQAREEAHR-  103
              ::::::::::    :::::::::::::::::::::::::::::::::::::::::::::
Db  1315  IERARSELQEKCTKLQQEAENITNQLEEAELKASAAVKSASNMESQLTEAQLLEETRQ  1374

Qy   104  ---LKCKMKTMEQIELLLQSQRSEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEAR  160
                 ::: ::::::  ::::::::::::::::::::::::::::::::: ::: : ::::
Db  1375  KIGLSSKLRQIESEKEALQEQLEEDDEAKRNY---ERKLAEVTTQMQEIKKKAEEDADLA  1431

Qy   161  KATGELADRLKKDLVSSRSKLKTL---NTELDQAKLELRSAQKD----LQSADQEITSLR  213
              ::::::::::::::::: ::::      :::::: :::::   :    ::::: :: :
Db  1432  KELEEGKRLNKDIEALERQVKELIAQNDRLDKSKRKKIQSELEDATIELEAQRTKVLELE  1491

Qy   214  KK  215
              ::
Db  1492  KK  1493
```

```
Query Match
Best Local Similarity   15.4%;   Score 166;   DB 2;   Length 2057;
                        25.2%;   Pred. No. 0.09;
Matches   61;   Conservative   47;   Mismatches   96;   Indels   38;   Gaps   8;

Qy     1 KTIINKLFDLAQEEENVLDAE--FLKNELDSVKAQLSQKDREKRDSQ----------AI 48
           |||| | | ||:|| : |    | ||| || || ||| ||  ||
Db  1303 KTVLEK------------AKGTLEAENADLATELRSVNSSRQENDRRKQAESQIAELQVKLAE 1354

Qy    49 IDTLRDTLEER------NATVESLQNALNKAEMLCSTLKKQMKFLEQRQDETKQRREEAHR- 103
         : | :       |:|     ||| ||  | || ||   || | |:|
Db  1355 IERARSELEQEKCTKLQQEAENITNQLEEAELKASAAVKSASNMESQLTEAQQLLEEETRQ 1414

Qy   104 --LKCKMKTMEQIELLLQSQRSEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEAR 160
            |   |:|:|:  : | | | ||| | |    ||:|:|:|
Db  1415 KLGLSSKLRQIESEKEALQEQLEDDDEARKNY---ERKLAEVTTQMQEIKKKAEEDADLA 1471

Qy   161 KATGELADRLRKKDLVSSRSKLKTL---NTELDQAKLELRSAQKD----LQSADQEITSLR 213
         | |:| |:|| ||  | |     |||    |   || | |:|
Db  1472 KELEEGKKRLNKDIEALERQVKELIAQNDRLDKSKKKIQSELEDATIELEAQRTKVLELE 1531

Qy   214 KK 215
         ||
Db  1532 KK 1533


RESULT 12
T47237
myosin II heavy chain [imported] - Naegleria fowleri (fragment)
C;Species: Naegleria fowleri
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: T47237
R;Shaw, D.R.; Sullivan, P.K.; Marciano-Cabral, F.; Ennis, H.L.
submitted to the EMBL Data Library, December 1995.
A;Description: Codon usage in Naegleria fowleri.
A;Reference number: Z24413
A;Accession: T47237
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-746  <SHA>
A;Cross-references: EMBL:U43192; PIDN:AAB01786.1
A;Experimental source: strain LEE mp; cell type amoeba

Query Match
Best Local Similarity   15.3%;   Score 164.5;   DB 2;   Length 746;
                        22.7%;   Pred. No. 0.039;
Matches   57;   Conservative   57;   Mismatches   104;   Indels   33;   Gaps   4;

Qy     1 KTIINKLFDLAQEEENVLDAEEFLKNELDSVKAQLSQKDREKRDSQAIIDTLRDTLEERN 60
Db   167 KQLQNELQNERTNLQKMKSENERLQRELEEMKRSLSDKQNESTSLDSKVYRSLEDKIRELT 226

Qy    61 ATVESLQNALNKAEMLCSTLKKQMKFLEQRQDETKQA-REEAHRLKCKMKTMEQIELLLQ 119
Db   227 ALLETERSSKTDLDKKRSKMDKEVKRLAQQLQETEQALKGETQKKNDADNRVKQLESELQ 286

Qy   120 SQRSEVEEMIRDMG-----------VGQSAVEQLAVYCVSLKKEYENLKEARKATGE 165
Db   287 GVKSERDRLRKDLNNTSGDMNGLKRQLDESNNLVAKLKAEIQKLQKDLSDHHGDREETEE 346

Qy   166 LADRLRKKDLVSSRSKL------------KTLNTELDQAKLELRSAQKDLQSAD-----Q 207
Db   347 QLDALRKQLQELTSRLSDANQKTQQEEAASRQNLESENNRLKSEVSRLREDLQENRRLKQ 406

Qy   208 EITSLRKKSDD 218
Db   407 EMERVQSESEN 417


RESULT 13
F96673
hypothetical protein F13O11.30 [imported] - Arabidopsis thaliana
```

```
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: F96673
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
A;Accession: F96673
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1313  <STO>
A;Cross-references: GB:AE005173; NID:g5042434; PIDN:AAD38273.1; GSPDB:GN00141
A;Genetics:
A;Gene: F13O11.30
A;Map position: 1

Query Match
Best Local Similarity   15.2%;   Score 163;   DB 2;   Length 1313;
                        22.8%;   Pred. No. 0.083;
Matches   67;   Conservative   52;   Mismatches   81;   Indels   94;   Gaps   9;

Qy    12 AQEEENVLD-----AEFLKNELDSVKAQL-SQKDREKRDSQAIIDTLRDTLEERNATVES 65
Db   182 AEEATKIAEIHAEKAEILASELGRLKALLGSKEEKEAIEGNEIVSKLK-------SEIEL 234

Qy    66 LQNALNKAEMLCSTLKKQMKFLEQRQDETKQAR------------------------EEA 101
Db   235 LRGELEKVSILESSLKEQEGLVEQLKVDLEAAKMAESCTNSSVEEKNKVHELEKEVEES 294

Qy   102 HRLKCK------------MKTM-----------------EQIELL---LQSQRSEVEEMIRDM 132
Db   295 NRSKSSASESMESVMKQLAELNHVLHETKSDNAAQKEKIELLEKTIEAQRIDLEEYGRQV 354

Qy   133 GVGQSAVEQLAVYCVSLKKEYE----------NLKEARKATGELAD------------- 168
Db   355 CIAKEEASKLENLVESIKSELEISQEEKTRALDNEKAATSNIQNLLDQRTELSIELERCK 414

Qy   169 ----RLKKDLVSSRSRKLKTLNTELDQAKLELRSAQKDLQSADQEITSLRKKSDD 218
Db   415 VEEEKSKKDMESLITLALQEASTESSEAKATLLVCQEELKNCESQVDSLKLASKE 468


RESULT 14
S67593
transport protein USO1 - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein D2552; protein YDL058w
C;Species: Saccharomyces cerevisiae
C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 21-Jul-2000
C;Accession: S67593; A38455; S30782
R;Bloecker, H.; Brandt, P.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S67587
A;Accession: S67593
A;Molecule type: DNA
A;Residues: 1-1790  <BLO>
A;Cross-references: EMBL:Z74106; NID:g1431058; PID:e253003; PID:g1431059; MIPS:YDL058
A;Accession: A38455
A;Molecule type: DNA
A;Residues: 1-1790
R;Nakajima, H.; Hirata, A.; Ogawa, Y.; Yonehara, T.; Yoda, K.; Yamasaki, M.
J. Cell Biol. 113, 245-260, 1991
A;Title: A cytoskeleton-related gene, USO1, is required for intracellular protein tra
A;Reference number: A38455; MUID:91185402
A;Accession: S30782
A;Molecule type: DNA
A;Residues: 1-389, 'TA', 392-724, 'S', 726-1790 <NAK>
A;Cross-references: GB:X54378; NID:g4777; PIDN:CAA38253.1; PID:g4778
A;Note: the authors translated the codon ACT for residue 768 as Ile
```

R;Hostetter, M.K.; Herman, D.J.; Bendel, C.M.; McClellan, M.; Tao, N.; Kendrick, K.E.
  submitted to the EMBL Data Library, February 1993
A;Description: An Integrin analogue in Saccharomyces cerevisiae.
A;Reference number: S30782
A;Accession: S30782
A;Molecule type: DNA
A;Cross-references:
A;Genetics:
A;Gene: SGD:USO1; INT1
A;Cross-references: SGD:S00002216; MIPS:YDL058w
A;Map position: 4L
C;Keywords: coiled coil; transmembrane protein
A;Cross-references: EMBL:L03188
F;71-846,'E',848-923,'K',925-1252,'I',1254-1318,'V',1320-1460,'S',1462-1580,'S
F;326-342/Domain: transmembrane #status predicted <TM1>
F;394-410/Domain: transmembrane #status predicted <TM2>
F;617-633/Domain: transmembrane #status predicted <TM3>

Query Match   15.2%;   Score 163;   DB 2;   Length 1790;
Best Local Similarity   23.7%;   Pred. No. 0.11;
Matches   51;   Conservative   57;   Mismatches   77;   Indels   30;   Gaps   7;

```
Qy     10  DLAQEENVLDAEFLKNELDSVKAQLSQKDREKRDSQAIIDTLRDTLEERNATVESLQNA    69
               :||:||  ||:|:||:|| :|: :|::      ::      :|: :|  |::|:
Db   1424  ELLEEKQNTIKS--LQDEI-----LSYKDKITRNDEKLLSIERDNKRD----LESLKEQ  1471

Qy     70  LNKAEMLCSTLKKQMKFLEQRQDETKQAREAHRLKCKMKTMEQIELLLQSQRSEVEEMI   129
           |   :| |  :        |||  :| ||: ::|:|::  |::  |  :  :
Db   1472  LRAAQESKARVEEGLLKKLEEESSKKEAELEKSKEM------MKKLESTIESNETELKSSM 1525

Qy    130  RDMGVGQSAVEQLAVYCVSLKKEYENLKEARKATGELADRL---KKDLVSSRSKLK---T   183
           | : |  |: |:|    |::|::  : :::   :  | |::     ||| :::|: :   |
Db   1526  ETIRKSDEKLEQ-----SKKSAEEDIKNLQHEKSDLISRINESEKDIEELKSKLRIEAK  1579

Qy    184  LNTELDQAKLELRSAQKDLQSADQEITSLRKKSDD   218
           ::|||  :: || :|::  : :::| |::
Db   1580  SGSELETVKQELNNAQEKIRINAEENTVLKSKLED  1614
```

RESULT 15
A26655
myosin heavy chain [similarity] - slime mold (Dictyostelium discoideum)
N;Contains: myosin ATPase (EC 3.6.1.32)
C;Species: Dictyostelium discoideum
C;Date: 05-Oct-1988 #sequence_revision 05-Oct-1988 #text_change 02-Feb-2001
A;Accession: A26655; A24728; S00250
R;Warrick, H.M.; De Lozanne, A.; Leinwand, L.A.; Spudich, J.A.
Proc. Natl. Acad. Sci. U.S.A. 83, 9433-9437, 1986
A;Title: Conserved protein domains in a myosin heavy chain gene from Dictyostelium disco
A;Reference number: A26655; MUID:87092266
A;Accession: A26655
A;Molecule type: DNA
A;Residues: 1-2116 <WAR>
A;Cross-references: GB:M14628; GB:M11938; NID:g167834; PIDN:AAA33227.1; PID:g167835
R;DeLozanne, A.; Lewis, M.; Spudich, J.A.; Leinwand, L.A.
Proc. Natl. Acad. Sci. U.S.A. 82, 6807-6810, 1985
A;Reference number: A24728; MUID:86016788
A;Accession: A24728
A;Molecule type: mRNA
A;Residues: 2035-2116 <DEL>
R;Wagle, G.; Noegel, A.; Scheel, J.; Gerisch, G.
FEBS Lett. 227, 71-75, 1988
A;Title: Phosphorylation of threonine residues on cloned fragments of the Dictyostelium
A;Reference number: S00250; MUID:88112226
A;Accession: S00250
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1734-1893 <WAG>
C;Comment: The rod domain is highly periodic, containing a pattern of 7-residue repeats
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Keywords: actin binding; ATP; coiled coil; hydrolase; nucleotide binding; P-loop; phos
F;1-818/Domain: globular head <HED>
F;89-747/Domain: myosin motor domain homology <MMOT>
F;179-186/Region: nucleotide-binding motif A (P-loop)
F;819-2116/Domain: alpha-helical rod <ROD>

Query Match   15.1%;   Score 162.5;   DB 2;   Length 2116;
Best Local Similarity   25.0%;   Pred. No. 0.15;
Matches   67;   Conservative   52;   Mismatches   86;   Indels   63;   Gaps   11;

```
Qy      5  NKLFFDLAQEEENVLDAE-FLKNELDSVKAQLSQKD---REKRDSQAIIDTLRDTLEERN    60
              :  | |::||:|||  | |:|::|    :| ||     ||: :::   : ::|:
Db    852  DKLEKSLKDTESNVLDLQRQLKAEKEFTLKAMYDSKDALEAQKRELEITRVEDMESELDEKK 911

Qy     61  ATVESLQN------------ALNKAEMLCSTLKKQMKFLEQRQDETKQAREAHRLKC   106
             :| ||:|            || :|:| |  |:| :  |::::::| :| :
Db    912  LALENLQNQKRSVEEKVRDLEEELQEEQKLRNTLEKLKKKYIEEELEEMKRVNDG------  965

Qy    107  KMKTMEQIELLLQSQRSEVEEMI------RDMGV------GQSAVEQLAVYCVS---   148
              :: ::| :  ::: :|:  |:      ||:|        ::|||:|
Db    966  QSDTISRLEKIRDELQKEVEELTESFSEESKDRGVLEKTRVRLQSELDDLTVRLDSETKD 1025

Qy    149  -----LKKEYENLKEARKA-TGELADRLKKDLVSSRSKLKTLNTELDQ------AKL   193
                |::: |:|:::| | | ||:    ::|: :  :: |  |::|      ||
Db   1026  KSELLRQKKLEEELKQVQEALAAETAAKLAQE--AANKKLQGEYTELNEKFNSEVTARS 1083

Qy    194  ELRSAQKDLQS----ADQEITSLRKKSD   217
           : :|:: : ::    | ::|  |:|::
Db   1084  NVEKSKKFTLESQLVAVNNELDEEKKNRD 1111
```

RESULT 16
A40997
myosin heavy chain, striated adductor muscle - scallop (Aequipecten irradians)
N;Contains: myosin ATPase (EC 3.6.1.32)
C;Species: Aequipecten irradians
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Jan-2001
A;Accession: A40997; S13557
R;Nyitray, L.; Goodwin, E.B.; Szent-Gyoergyi, A.G.
J. Biol. Chem. 266, 18469-18476, 1991
A;Title: Complete primary structure of a scallop striated muscle myosin heavy chain.
A;Reference number: A40997; MUID:92011595
A;Accession: A40997
A;Molecule type: mRNA
A;Residues: 1-1938 <NYI>
A;Cross-references: GB:X55714; NID:g95611; PIDN:CAA39247.1; PID:g95612
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Keywords: actin binding; ATP; coiled coil; hydrolase; muscle contraction; nucleotid
F;86-763/Domain: myosin motor domain homology <MMOT>
F;176-183/Region: nucleotide-binding motif A (P-loop)
F;547-586/Region: actin binding #status predicted
F;653-675/Region: actin binding #status predicted
F;836-1938/Domain: coiled coil #status predicted <COI>
F;1277-1938/Region: S2
F;182/Binding site: ATP (Lys) #status predicted
F;693,703/Active site: Cys #status predicted

Query Match   15.1%;   Score 162;   DB 1;   Length 1938;
Best Local Similarity   24.5%;   Pred. No. 0.14;
Matches   73;   Conservative   50;   Mismatches   89;   Indels   86;   Gaps   12;

```
Qy      1  KTIINKLFFD---------LAQEEENVLDAEFLKNELDSVKAQL------------SQK    38
              |:: ||:|         || :::::|  :  ::|: :| |:            |::
Db    904  KLIMQKRADFESQIKELEERLLDEEDAAADLEGIKKKMEADNANLKRDIGDLENTLQKAEQ  963

Qy     39  DREKRDSQAIIDTL--------RDTLEERN-ATVESLQ-----NALNKAE    74
           |  |:|:|   ::|        :: | ::| ::  :|:     ||:||
Db    964  DKAHKDNQ--ISTLQGEISQODEHIGKLNKEKKALEEANKKTSDSLQAEEDKCNHLNK-- 1019

Qy     75  MLCSTLKKQMKFLEQRQDETKQAREAHRLKCKMK----TMEQIELLLQSQRSEVEEMI   129
            | :|:|: :  ||:: ::: :: |: :::: ::    | ::: :|:::::  ::|::
Db   1020  -LKAKLEQALDELEDNLEREKKVRGDVEKAKRKVEQDLKSTQENVEDLERVKR-ELEENV 1077
```

```
Qy   130 R---------------------DMGVGQSAVEQLAVYCVSLKKEYENLKEARKATGELADRLKKDLVSSR 178
             ||  ::| |:|| :| |||
Db  1078 RRKEAEISSLNSKLEDEQNLVSQLQRKIKELQARIEELEEELEAERNARAKVEKQRAELN 1137

Qy   179 SKLKTLNTELDQA------------------KLELRSAQKDLQSA----DQEITSLRKKSDD 218
             ||||
Db  1138 RELEELGERLDEAGGATSAQIELNKKREAELLKIRRDLEEASLQHEAQISALRKKHHOD 1195
```

smooth muscle myosin heavy chain isoform SM2 - human (fragment)
A;Accession: I52860
A;Reference number: I52860
A;Title: Human smooth muscle myosin heavy chain isoforms as molecular markers for vascul
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
A;Cross-references: GB:S67238; NID:g452982; PIDN:AAB28950.1; PID:g452983
A;Residues: 1-296 <RES>
A;Molecule type: mRNA
A;Status: preliminary; translated from GB/EMBL/DDBJ
Circ. Res. 73, 1000-1012, 1993
R;Aikawa, M.; Sivam, P.N.; Kuro-O, M.; Kimura, K.; Nakahara, K.; Takewaki, S.; Ueda, M.;
C;Accession: I52860
C;Species: Homo sapiens (man)
I52860
RESULT 17

Query Match   15.0%; Score 161; DB 2; Length 296;
Best Local Similarity   23.8%; Pred. No. 0.023;
Matches   60; Conservative   52; Mismatches   92; Indels   48; Gaps   9;

```
Qy    10 DLAQEENVLDAEFLKNELDSVKAQLSQK--------------------DREKRDSQAIIDTLRDTLEE 58
             |:|:|:||| || :|  |:   |                       || |||:|| ||| |||
Db    46 DLMQLQEDLAAAEBARKQAADLEKEELASSLSGRNALQDEKRLEARIAQLEEELEE 105

Qy    59 RNATVESLQNALNK-------AEMLC---------STLKKQMKFLEQRQDETKQAREAHRL-- 104
             | |  ||:|| |       |||:             |||:|||||||||||||:: |||
Db   106 EOGNMEAMSDRVRKATQQAEQLSNELATERTTAQKNESARQQLERQNKELRSKLHEMEGA 165

Qy   105 -KCKMK-TMEQIELLLQSQRSEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKA 162
               ||||  ||||||||:|::|||||:||:||||||||||||||||||||||||||||||
Db   166 VKSKFKSTIAALEAKIAQLEEQVQEQAEREK--QAATKSLKQKDKLKEILLQVEDERK- 221

Qy   163 TGELADRLKKDLVSSRSKLKTLNTELDQAKLE-----LRSAQKDLQSADQ------E 208
             |||||||||||||||:::||||||||||||       | |||||||| |       |
Db   222 ---MAEQVKEQAEKGNAGVKQLRKQLEBAEEESQRINANRRKLQORELDEATESNEAMGRE 278

Qy   209 ITSLRKKSDDPP 220
             ::|| ||
Db   279 VNALKSKLRGPP 290
```

RESULT 18
JH0720

tanabin - African clawed frog
A;Accession: JH0720
A;Reference number: JH0720; MUID:92398961
A;Title: A protein expressed in the growth cones of embryonic vertebrate neurons defines
C;Superfamily: myosin
A;Cross-references: GB:M99387; NID:g214816; PIDN:AAA49966.1; PID:g214817
A;Residues: 1-1744 <HEM>
A;Molecule type: mRNA
A;Status: preliminary
C;Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 21-Jul-2000
C;Accession: JH0720
Neuron 9, 417-428, 1992
R;Hemmati-Brivanlou, A.; Mann, R.W.; Harland, R.M.
C;Species: Xenopus laevis (African clawed frog)

Query Match   14.9%; Score 160.5; DB 2; Length 1744;
Best Local Similarity

Matches   57; Conservative   58; Mismatches   71; Indels   49; Gaps   8;

```
Qy    12 AQEEENVLDAEFLKNELDSVKAQLSQKDREKRDSQAIIDTLRDTLEERNATVESLQNALN 71
             |:|:|:||||||| || |||:|:||
Db    33 ALEEEN----ELLRKEIHSLRSSKSSERCWKKKHHEEMM-KLRDALDDGH------REMV 80

Qy    72 KAEMLCSTLKKQMKFLEQRQDETKQAREAHRLKCKMKTMEQIELLLQSQR---------- 122
             |:|| ||:|||:|||||||||||||||||||::|      ||||||||:||
Db    81 QAEMVRDSIYEEIEPVKQRCLEEKQAREDA-----KKELSESKLLEEETRAQIMLKERL 135

Qy   123 ----SEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKA-----------TGELADR 169
             :| |:|:| |||||||||||||||||||||||||          | ::|
Db   136 GQLEAELEDILRDHEEKALMEE---EIASFSQRLENFRVAPVAFKPVEVDDYARKLSEI 192

Qy   170 LKKDLVSSRSKLKTLNTELDQAKLELRSAQKD---------------LQSADQEITSLRKKSD 217
             ||:||||||||||||||||| |||:|| :| |              ||| |||||||||||
Db   193 WQGAVEEYKSEVSVLEAGLSESKENLRKVLEENKQNRLLLQSLDKELVSLKMRKE 247
```

RESULT 19
A59294

skeletal myosin - nematode (Onchocerca volvulus)
A;Alternate names: major body wall myosin
N;Contains: myosin ATPase (EC 3.6.1.32)
A;Accession: A59294
A;Reference number: A59294; MUID:92158005
A;Title: Comparison of the body wall myosin heavy chain sequences from Onchocerca vol
Mol. Biochem. Parasitol. 50, 255-260, 1992
R;Werner, C.; Rajan, T.V.
C;Accession: A59294
C;Superfamily: myosin heavy chain; myosin motor domain homology
A;Experimental source: sex female
A;Cross-references: GB:M74066; NID:g159892; PIDN:AAA29420.1; PID:g159893
A;Residues: 1-1957 <WER>
A;Molecule type: mRNA
A;Status: preliminary; not compared with conceptual translation
F;87-773/Domain: myosin motor domain homology <MMO>
C;Species: Onchocerca volvulus

Query Match   14.9%; Score 160.5; DB 2; Length 1957;
Best Local Similarity   21.5%; Pred. No. 0.17;
Matches   59; Conservative   56; Mismatches   83; Indels   77; Gaps   10;

```
Qy    10 DLAQEEENV-LDAEFLKNELDSVKAQLSQKDREKRDSQAIIDTLRDTLEERNATVESL-- 66
             ||||:|:| ||||||| ||:|:||||||:||:|| |||:|| ||| ||||:
Db    10 DLSRSRKKIENDVENLKKSIAELETRLQKTDADKQSREQOIRTLQDEMQQQDENIAKLNK 1001

Qy    67 ----QNALNKAEM------------LCSTLKKQMKFLEQRQDETKQAREAHR---- 103
             ||||:|                 ||:|||:|||||||||||||||||||
Db   942 DLSRSKKKKIENDVENLKKSIAELETRLQKTDADKQSREQOIRTLQDEMQQQDENIAKLNK 1001

Qy   104 ---LCKKMKTMEQIELLLQSQRSEVEEMIRD-----------------MGVGQSAVEQ 141
             |:||||||||||||||:|:|:|||||||
Db  1002 EKKHQEEINRKLMEDLQVEEDKGNYSNKLKGKLEQSLDDLEDNLEREKRGNEIEKQKRK 1061

Qy   142 LAVYCVSLKKEYENLKEARKATGELADRLKKDLVSSRSKLKTLNTELDQ--------- 190
             || | | ||||||||||||||||||||||||||||||||||||||
Db  1062 IGGELKVAQENMEEIE---RORHEIESNLKKEFEAQAITARLEEEQDLVGKLKKQVNE 1117

Qy   191 ----AKLELRSAQKDLQSA----DQEITSLRKKSDD 218
             ||:|| :| |              ||||||||||
Db  1118 TQNRITELEELENERQSRSK---AERAKSDL---QRELELGDRLDEQGGATAAQVEV 1170
```

RESULT 20
MKKW

myosin heavy chain B [similarity] - Caenorhabditis elegans
N;Contains: myosin ATPase (EC 3.6.1.32)
C;Date: 13-Jun-1983 #sequence_revision 19-May-2000 #text_change 19-Jan-2001
C;Accession: T20770; T21629; A93958; A93387; A21074; A02992
R;Kershaw, J.
C;Species: Caenorhabditis elegans

```
Qy   191 ---AKLELRSAQKDLQSA----DQEITSLRKKSDD 218
             ||:|| :| |              ||||||||||
Db  1171 NKKREAELAKIRRDLEEAANMHHENQLAAIRKKHND 1205
```

submitted to the EMBL Data Library, November 1996
A;Reference number: Z19322
A;Accession: T20770
A;Molecule type: DNA
A;Status: translated from GB/EMBL/DDBJ
A;Residues: 1-1963 <WIL>
A;Experimental source: EMBL:Z81499; PIDN:CAB04089.1; GSPDB:GN000019; CESP:F1IC3.3
A;Cross-references: EMBL:Z81499; PIDN:CAB04089.1; GSPDB:GN000019; CESP:F1IC3.3
A;Accession: T21629
A;Molecule type: DNA
A;Status: translated from GB/EMBL/DDBJ
A;Residues: 1-1963 <WI2>
A;Cross-references: EMBL:Z83107; PIDN:CAB05505.1; GSPDB:GN000019; CESP:F1IC3.3
A;Experimental source: clone F32A7
R;Karn, J.; Brenner, S.; Barnett, L.
Proc. Natl. Acad. Sci. U.S.A. 80, 4253-4257, 1983
A;Title: Protein structural domains in the Caenorhabditis elegans unc-54 myosin heavy ch
A;Accession: A93958
A;Molecule type: DNA
A;Residues: 1-61, EMSVIQ/,65-376,'v',378-1963 <KAR>
R;Hasegawa, K.; Arakawa, E.; Oda, S.; Matsuda, Y.
R;McLachlan, A.D.; Karn, J.
Nature 299, 226-231, 1982
A;Title: Periodic charge distributions in the myosin rod amino acid sequence match cross
A;Reference number: A93287; MUID:82272395
A;Accession: A93287
A;Molecule type: DNA
A;Residues: 847-1333,'R',1335-1876,'L',1878-1963 <MCL>
R;Wills, N.; Gesteland, R.F.; Karn, J.; Barnett, L.; Bolten, S.; Waterston, R.H.
Cell 33, 575-583, 1983
A;Introns: 21/3; 64/3; 111/3; 264/1; 525/3; 951/2; 1747/3; 1819/3; 1894/3
A;Superfamily: myosin heavy chain; myosin motor domain homology
C;Keywords: actin binding; ATP; coiled coil; hydrolase; methylated amino acid; muscle co
A;Title: The genes sup-7 X and sup-5 III of Caenorhabditis elegans suppress amber nonsen
A;Reference number: A21074; MUID:83232892
A;Accession: A21074
A;Molecule type: DNA
A;Residues: 1873-1963 <WI3>
A;Cross-references: GB:V01494; NID:g6783; PIDN:CAA24738.1; PID:g6784
C;Genetics:
A;Gene: unc-54; CESP:F1IC3.3
A;Map position: 1
F;125/Modified site: N6,N6,N6-trimethyllysine (Lys) #status predicted
F;180/Binding site: ATP (Lys) #status predicted
F;702,712/Active site: Cys #status predicted

F;1163-1963/Region: light meromyosin
F;848-1102/Region: coiled coil #status predicted <COI>
F;848-1963/Domain: actin binding #status predicted
F;766-780/Region: actin binding #status predicted
F;662-684/Region: actin binding #status predicted
F;174-181/Region: nucleotide-binding motif A (P-loop)
F;84-775/Domain: myosin motor domain homology <MMOT>

Query Match 14.9%; Score 160.5; DB 1; Length 1963;
Best Local Similarity 25.1%; Pred. No. 0.17;
Matches 59; Conservative 41; Mismatches 78; Indels 57; Gaps 9;

Qy 3 IINKLFFDLAQEEENVLDAEFLKNELDSVKAQLSQKDREKRDSQAIIDTLRDTLEE 62
  : || |:||: :| ::| | ||| || | :: | | | |
Db 1011 INRKLMEDLQSEEDK---------GNHQNKVKAKLEQ------------TLDDLEDSLRERKRA 1053

Qy 63 VESLQNALNKAEMLCSTLKKQMKFLEQRQDET-KQAREEAHRLKCKMKTMEQIELLLQSQ 121
  :: ||| ::| ||| |: | | | | : : | :
Db 1054 RADLDKQRRKVE------GELKIAQENIDESGRQRHDLENNLKKKESELHSVSSRLEDE 1106

Qy 122 RSEVEEMIRDMGVGQSQSAVEQLAVYCVSLKKEYENLKEARKATGELADRLKKDLVSSRSKL 181
  :: |:|: | ||| || | || | |:
Db 1107 QALVSKLQRIKDQSRISE-------LEEELENERQSRSK----ADRAKSDL--QREL 1152

Qy 182 KTLNTELDQ------------------------------AKLELRSAQKDLQSA----DQEITSLRKKSDD 218
  : | | :|| :: || :||: |||| |

Db 1153 EELGEKLDEQGGATAAQVEVNKKREAELAKLRRDLEEANMNHENQLGGLRKKHTD 1207

RESULT 21
JC5420
smooth muscle myosin heavy chain 1 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 02-Feb-2001
C;Accession: JC5420
R;Hasegawa, K.; Arakawa, E.; Oda, S.; Matsuda, Y.
Biochem. Biophys. Res. Commun. 232, 313-316, 1997
A;Title: Molecular cloning and expression of murine smooth muscle myosin heavy chains
A;Reference number: JC5420; MUID:97242182
A;Accession: JC5420
A;Molecule type: mRNA
A;Residues: 1-1972 <HAS>
C;Cross-references: DDBJ:D85923; NID:g1945077; PIDN:BAA19690.1; PID:g1945078
A;Experimental source: smooth muscle
C;Comment: This protein plays a role in smooth muscle cell contraction.
A;Superfamily: myosin heavy chain; myosin motor domain homology
C;Keywords: nucleotide binding; P-loop
F;88-771/Domain: myosin motor domain homology <MMOT>
F;178-185/Region: nucleotide-binding motif A (P-loop)

Query Match 14.9%; Score 160; DB 2; Length 1972;
Best Local Similarity 22.3%; Pred. No. 0.19;
Matches 55; Conservative 53; Mismatches 91; Indels 48; Gaps 7;

Qy 10 DLAQEEENVLDAEFLKNELDSVKAQLSQK-----------DREKRDSQAIIDTLRDTLEE 58
  | |:|| ||| : | ||| |:: | ||| || |
Db 1688 DLMQLQEDLAAAERARKQADLEKEELAEELASSLSGRNTLQEDKRRLEARIAQLEEELEE 1747

Qy 59 RNATVESLQNALNKAEMLCSTLKKQMKFLEQRQDETKQAREEAHR------------ 103
  :|:: :| || |: | | | : :|
Db 1748 EQGNMEAMSDRVRKATLQAEQLSNELATERSTAQKNESAARQLERQNKELRSKLQEVEGA 1807

Qy 104 LKCKMK-TMEQIELLLQSQRSEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKA 162
  |: |: : ||| : | | | || || | ||
Db 1808 VKAKLKSTVAALEAKIAQLEEQVEQEAREK---QAATKSLKQKDKKLKEVLLQVEDERK- 1863

Qy 163 TGELADRLKKDLVSSRSKLKTLNTELDQAKLE----------LRSAQKDLQSADQ------E 208
  || | :| | : | | ||
Db 1864 ---MAEQYKEQAEKGNTKVKQLKRQLEEAEEESQCINANRRKLQRELDEATESNEAMGRE 1920

Qy 209 ITSLRKK 215
  ::|: |
Db 1921 VNALKSK 1927

RESULT 22
A41919
kinesin heavy chain - human
N;Contains: kinesin ATPase (EC 3.6.1.-)
C;Species: Homo sapiens (man)
C;Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 19-Jan-2001
C;Accession: A41919; S24603
R;Navone, F.; Niclas, J.; Hom-Booher, N.; Sparks, L.; Bernstein, H.D.; McCaffrey, G.;
J. Cell Biol. 117, 1263-1275, 1992
A;Title: Cloning and expression of a human kinesin heavy chain gene: Interaction of t
A;Reference number: A41919; MUID:92299683
A;Accession: A41919
A;Molecule type: mRNA
A;Status: nucleic acid sequence not shown
A;Residues: 1-963 <NAV>
A;Cross-references: GB:X65873; NID:g34082; PIDN:CAA46703.1; PID:g34083
C;Genetics:
A;Gene: GDB:KNS1; KNS
A;Cross-references: GDB:135352
A;Superfamily: kinesin heavy chain; kinesin motor domain homology
C;Keywords: ATP; coiled coil; heterotetramer; hydrolase; microtubule binding; nucleot
F;9-331/Domain: kinesin motor domain homology <KMOT>
F;85-92/Region: nucleotide-binding motif A (P-loop)

```
F;402-860/Domain: rod #status predicted <RDD>
F;861-963/Domain: globular #status predicted <GBD>
F;91/Binding site: ATP (Lys) #status predicted

Query Match          14.8%;    Score 159; DB 1; Length 963;
Best Local Similarity  24.2%;  Pred. No. 0.1;
Matches  57; Conservative  48; Mismatches  93; Indels  38; Gaps  6;

Qy    10 DLAQEE-ENVLDAEFLKNELDSVKAQLSQKDREKRDSQAIIDTLRDTLEERNATVESLQN 68
         :||:|| |||||||||||||||:|::|| ||::|||||||||||:||||||::||:|
Db   482 DASKEVKEVLQA-----LEELAVNYDQKSQEVEDKTKEYELLSDELNQKSATLASIDA 535

Qy    69 A-LNK------------------AEMLCSTLK--------------KQMKFLEQRQDETKQAREEAH 102
         | |||                   ||:||:|               :|::| |
Db   536 ELQKLKEMTNHQKRAAEMMASLLKDLAEIGIAVGNNDVKQPEGTGMIDEEFTVARLYIS 595

Qy   103 RLKCKMKTM----EQIELLLQSQRSEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKE 158
         ||:|:|:||    ||||||||||||||||||||||||||||||||||||||||:|||:
Db   596 KMKSEVKTWVKRCKQLESTQTESNKKMEENEKELAACQLRISQHEAKIKSLTEYLONVEQ 655

Qy   159 ARKATGELADRLKDLVSSRSKLKTLNTELDQAKLELRSAQKDLQSADQEITSLRK 214
         :|:| |||:|||||||||||||||||||||||:||||||||||||:|||||||
Db   656 KKRQLEESVDALSEELVQLRAQEKVHEMEKEHLN-KVQTANEVKQAVEQIQSHRE 710
```

RESULT 23
A41604
myosin heavy chain, smooth muscle, long splice form - rabbit
N;Contains: myosin ATPase (EC 3.6.1.32)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Jan-2001
C;Accession: A41604; A33501
R;Babij, P.; Kelly, C.; Periasamy, M.
Proc. Natl. Acad. Sci. U.S.A. 88, 10676-10680, 1991
A;Title: Characterization of a mammalian smooth muscle myosin heavy-chain gene: complete
A;Reference number: A41604; MUID:92073350
A;Accession: A41604
A;Molecule type: mRNA
A;Residues: 1-1972 <BAB>
A;Cross-references: GB:M77812
R;Nagai, R.; Kuro-o, M.; Babij, P.; Periasamy, M.
J. Biol. Chem. 264, 9734-9737, 1989
A;Title: Identification of two types of smooth muscle myosin heavy chain isoforms by cDN
A;Reference number: A33501; MUID:89255535
A;Accession: A33501
A;Molecule type: mRNA
A;Residues: 1455-1972 <NAG>
A;Cross-references: GB:J04833; NID:g165519; PIDN:AAA31407.1; PID:g165520
A;Experimental source: smooth muscle
A;Note: examination by Southern blotting for the regions of difference between this isof
ative splicing
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Keywords: actin binding; alternative splicing; ATP; coiled coil; hydrolase; methylated
A;Domain: myosin motor domain homology <MMOT>
F;88-771/Domain: myosin motor domain homology <MMOT>
F;178-185/Region: nucleotide-binding motif A (P-loop)
F;559-572/Region: actin binding #status predicted
F;633-647/Region: actin binding #status predicted
F;844-1938/Domain: coiled coil #status predicted
F;844-1284/Region: S2
F;1285-1972/Region: light meromyosin
F;1939-1972/Domain: carboxyl-terminal <CBT>
F;129/Modified site: N6,N6,N6-trimethyllysine (Lys) #status predicted
F;184/Binding site: ATP (Lys) #status predicted
F;701,711/Active site: Cys #status predicted

```
Query Match          14.8%;    Score 159; DB 1; Length 1972;
Best Local Similarity  22.8%;  Pred. No. 0.21;
Matches  56; Conservative  52; Mismatches  91; Indels  48; Gaps  7;

Qy    10 DLAQEENVLDAEFLKNELDSVKAQLSQK------DREKRDSQAIIDTLRDTLEE 58
         ||| || ||:|||:||||||||||||||      ||||||||||||||||||
Db  1130 EKQKRDLGEELEALKTELEDLTDSTAAQELRSKREQEVNILKKTLEEEAKTHEAQIQEM 1189
```

```
Db  1688 DLMQLOEDLAAAERARKQADLEKEELAEELASSLSGRNALQDEKRRLEARIAQLEEELEE 1747
         ||:|:|:||:||:|:| ||||:|:|||| |
Qy    59 RNATVESLQNALNK-----AEMLCSTLKKQMKFLEQRQDETKQAREEAHRLCKCMKTME-- 112
Db  1748 EQGNMEAMSDRVRKATQQAAEQLSNELATERSTAQKNESARQLERQNKELKSKLQEMEGA 1807

Qy   113 --------QIELLLQSQRSEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKA 162
         ||||:|::|:|::|| ||:|| |:| |
Db  1808 VKSKFKSTIAALEAKIAQLEEDVQEQAREK----QAAKALKQRDKKLIKEMLQVEDERK- 1863

Qy   163 TGELADRLKDLVSSRSRSKLKTLNTELDQAKLE----LRSAQKDLQSADQ------E 208
         ||:|:|:| :|:| |||||||||||:|::|    |||||||||:| |
Db  1864 ---MAEQYKEQAEKGNAKVKQLKRQLEEAEESQRINANRRKLQRELDEATESNEAMGRE 1920

Qy   209 ITSLRKK 215
         ::|||:|
Db  1921 VNALKSK 1927
```

RESULT 24
S21801
myosin heavy chain, neuronal [similarity] - rat
N;Alternate names: myosin II
N;Contains: myosin ATPase (EC 3.6.1.32)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Jan-2001
A;Accession: S21801
A;Molecule type: mRNA
A;Residues: 1-1999 <SUN>
A;Cross-references: EMBL:X62659
R;Sun, W.; Chantler, P.D.
Biochem. Biophys. Res. Commun. 175, 244-249, 1991
A;Title: A unique cellular myosin II exhibiting differential expression in the cerebr
A;Reference number: PN0013; MUID:91151356
A;Accession: PN0013
A;Molecule type: mRNA
A;Residues: 1914-1998, 'I' <SU2>
A;Experimental source: brain
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Keywords: actin binding; ATP; coiled coil; hydrolase; methylated amino acid; nucleo
A;Domain: myosin motor domain homology <MMOT>
F;84-763/Domain: myosin motor domain homology <MMOT>
F;174-181/Region: nucleotide-binding motif A (P-loop)
F;541-575/Region: actin binding #status predicted
F;653-675/Region: actin binding #status predicted
F;836-1999/Domain: coiled coil #status predicted
F;836-1276/Region: S2
F;1277-1999/Region: light meromyosin
F;125/Modified site: N6,N6,N6-trimethyllysine (Lys) #status predicted
F;180/Binding site: ATP (Lys) #status predicted
F;693/Binding site: Cys #status predicted
F;1916/Binding site: phosphate (Ser) (covalent) #status predicted
F;1943/Binding site: phosphate (Ser) (covalent) #status predicted

```
Query Match          14.7%;    Score 158.5; DB 1; Length 1999;
Best Local Similarity  20.3%;  Pred. No. 0.23;
Matches  62; Conservative  65; Mismatches  88; Indels  91; Gaps  9;

Qy     4 INKLFEDLAQEENV------------LDAEFF-LKNELDSVKAQLSQK 38
         |:| | ||||||          |||:| |||||||||||||||
Db  1070 IAELKMQLAKKEELQAALARVEEEAQKNMALKKIRELESQISELQEDLESERASRNKA 1129

Qy    39 DREKRDSQAIIDTLRDTLEERNATVESLQNALNKAEMLCSTLKK------------QMKFLEQ 89
         |:|||:|||||||||||||||||| ::||| || |||||||||            |||||||
Db  1130 EKQKRDLGEELEALKTELEDLTDSTAAQELRSKREQEVNILKKTLEEEAKTHEAQIQEM 1189

Qy    90 RQDETKQAREEAHRL---KCKMKTME---------------QIELLLQS-----QRSEV 125
         ||:|||||| |:|    |||||||               ::||||||     |||||
Db  1130 RQDETKQAREEAHRL---KCKMKTME---------------QIELLLQS-----QRSEV 125
```

```
Db  1190 RQKHSQAVEELAEQLEQOTKRKVANLEKAKQTLENERGELANEVKVLLQGGRDSEHKRKKV 1249
Qy   126 EEMIRDMGV-----GQSAVEQLAVYCVSLKKEYENLKEARKATGELADRLKKDLVSSRSKL 181
Db  1250 EAQLQELQVKPNEGERRVTELADKVTKLQVELDNVTGLLSQSDSDSKSSKLTKDFSALESQL 1309

Qy   182 K-------------TLNTELDQAKLELRSAQKDLQSADQE----------------ITSL 212
Db  1310 QDTQELLQEENRQKLSLSTKLKQVEDDEKNSFREQLEEEEEAKHNLEKQIATLHAQVADM 1369

Qy   213 RKKSDD 218
Db  1370 KKKMED 1375
```

RESULT 25
H69378
conserved hypothetical protein AF1032 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 02-Feb-2001
C;Accession: H69378
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae
A;Reference number: A69250; MUID:98049343
A;Accession: H69378
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-886 <KLE>
A;Cross-references: GB:AE001032; GB:AE000782; NID:g2689355; PIDN:AAB90211.1; PID:g264956
C;Superfamily: Archaeoglobus fulgidus conserved hypothetical protein AF1032

Query Match   14.7%; Score 157.5; DB 2; Length 886;
Best Local Similarity 22.3%; Pred. No. 0.11;
Matches 56; Conservative 71; Mismatches 83; Indels 41; Gaps 9;

```
Qy    1 KTIINKLFFDLAQEEENVLDAEFLIKNELDSVKAQ--------------LSQKDRE-KRDSQAII 49
           || ||               |:||    |:       ||          |:
Db  207 ESLREKLSEEVRNLESRLKELEEHKSRLESLRKQESSVLQEVRGLEEKLRELEKQLKEVV 266

Qy   50 DTFLRDTLEERNATVESLQNALNK--------AEMLCSTLKKQMKFLEQR------ODETK 95
           |::|| ||               |  |:||| || | |:              |||
Db  267 ERIED-LEKKAKEVKELKPRAERYSILEKLLSEINQALRDVEKREGDLTREAAGIQAQLK 325

Qy   96 QAREEAHRLKCKMKTMEQIE---------LLLQSQRSEVEEMIRDMGVGQSAVEQLAVV 145
           |                   |:|| |:||  ||| ||| || |:|
Db  326 KAEEDNSKLEEITKRIEELERELEREFEKSHRLLETLKPKMDRM---QGI-KAKLEEKNLT 381

Qy  146 CVSLKKEYENLKEARKATGELADRLKKDLVSSRSRSKLKTLNTELDQAKLELRSAQKDLQSA 205
          |:  |       |  :|               |:|| |:||| ||||||| ||||||
Db  382 PDKVEKMYDLLSKAKEEKEITEKLKK-LIAKKSSLKTRGAQLKKAVEELKSAERTCPVC 440

Qy  206 DQEITSLRKKS 216
          || ||||
Db  441 GRELDEEHRKN 451
```

RESULT 26
I8473
kinesin heavy chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
C;Accession: I8473
R;Gudkov, A.V.; Kazarov, A.R.; Thimmapaya, R.; Axenovich, S.; Mazo, I.A.; Roninson, I.B.
Proc. Natl. Acad. Sci. U.S.A. 91, 3744-3748, 1994
A;Title: Cloning mammalian genes by expression selection of genetic suppressor elements
A;Reference number: I49673; MUID:94224818
A;Accession: I8473

A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-881 <RES>
A;Cross-references: GB:L27153; NID:g468354; PIDN:AAA20133.1; PID:g468355
A;Genetics:
A;Gene: Khcs
C;Superfamily: kinesin heavy chain; kinesin motor domain homology
F;9-331/Domain: kinesin motor domain homology <KMOT>

Query Match   14.7%; Score 157.5; DB 2; Length 881;
Best Local Similarity 24.2%; Pred. No. 0.12;
Matches 57; Conservative 48; Mismatches 93; Indels 38; Gaps 6;

```
Qy   10 DLAQEE-ENVLDAEFLIKNELDSVKAQLSQKDREKRDSQAIIDTFLRDTLEERNATVESLQN 68
          |                |:|| |:                  |:|| |:|
Db  482 DASKEEVKEVLQA----------LEELAVNVDQKSQEVEDKTKEYELLSDELNQKSATLIASTDA 535

Qy   69 ALNK------AEMLCSTLK--------------KQMKFLEQRQDETKQAREEAH 102
          |       || | |                  ||||| ||
Db  536 ELQKLKEMTNHQKKRAAEMAASLLKDLAEGIAVGNNDVKQPEGTGMIDEEFTVARLYIS 595

Qy  103 RLKCKMKTM----EQIELLLQSQRSEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKE 158
          | |          ||||| |  || || ||| || |:|
Db  596 KMKSEVKTMVKRCKQLESTQTTESNKKMEENEKELAACQLRISQHEARKIKSLTEYLQNVEQ 655

Qy  159 ARKATGELADRLKKDLVSSRSKLKTLNTELDQAKLELRSAQKDLQSADQEITSLRK 214
          |||| ||||| |:|:                 |:|| |:||| |||||
Db  656 KKRQLEESVDSLGEELVQLRAQEKVHEMEKEHLN-KVQTANEVKQAVEQIQSHRE 710
```

RESULT 27
S06117
myosin heavy chain, nonmuscle (clone lambda-FMHC) - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 20-Jun-2000
s.
A;Reference number: S06116; MUID:90032648
A;Accession: S06117
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-924 <KAT>
A;Accession: S06117
R;Katsuragawa, Y.; Yanagisawa, M.; Inoue, A.; Masaki, T.
Eur. J. Biochem. 184, 611-616, 1989
C;Species: Gallus gallus (chicken)
A;Note: this translation is not annotated in GenBank entry GGMHCFC, release 114
A;Cross-references: GB:X17590
A;Superfamily: myosin heavy chain; myosin motor domain homology
F;1-303/Domain: myosin motor domain homology <MMOT>
A;Title: Two distinct nonmuscle myosin-heavy-chain mRNAs are differentially expressed

Query Match   14.6%; Score 157; DB 2; Length 924;
Best Local Similarity 21.3%; Pred. No. 0.12;
Matches 65; Conservative 58; Mismatches 92; Indels 90; Gaps 10;

```
Qy    4 INKLFFDLAQEEENV---------------------LDAEF--LKNELDSVKAQLSQK 38
          |||| ||                          |:|||      |:|| |:|
Db  610 IEELKIQLAKKEEELQAALARGDEEAVQKNNALKVIRELQQIAELQEDLESSEKASRNKA 669

Qy   39 DREKRDSQAIIDTFLRDTLEERNATVESLQNALNKAEMLCSTLKK--------QMKFL 87
          || |:| |:                |:||| |:|||  || |          ||||
Db  670 EKQKRDLSEELEALKTELEDTLDTTAAQELRTKREQEVEALKKAIEEETKNHEAQIQEI 729

Qy   88 EQRQ----DETKQAREEAHRLK--------------CKMKTMEQIELLLQSQR-- 122
          |:|       |:|| ||||| |                 || | |||| |
Db  730 RQRHATAELEELSEQLEQAKRFKANLERKNQGLESDNKELACEVKVLQQVKAESEHRRKL 789

Qy  123 -SEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYEN----LKEARKA--------- 162
          ||| || ||| || |:|             :||       |:||
Db  790 DAQVQELTAKVTEGERLRVELAEKANKLQNELDNVSSLEEAEKGIKFAKDAASLESQL 849

Qy  163 -TGELADRLKKDLVSSRSKLKTLNTE----LDQAKLELRSAQKDLQ----SADQEITSLR 213
```

Db 850 QDTQELLQEETRQKLNLSSRIQLEEEKNNLQEQEEEEARKNLEKQMLALQAQLAEAK 909
         ::: |::|: |||: | |||| ||||::| | |: |: | ::|::: :
Qy 214 KKSDD 218
        ||||
Db 910 KKVDD 914

RESULT 28
T14867
Interaptin - slime mold (Dictyostelium discoideum)
C;Species: Dictyostelium discoideum
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 11-May-2000
A;Accession: T14867
R;Rivero, F.J.; Kuspa, A.; Brokamp, R.; Matzner, M.; Noegel, A.A.
J;Cell Biol. 142, 735-750, 1998
A;Title: Interaptin, an actin-binding protein of the alpha-actinin superfamily in Dictyo
ts.
A;Reference number: Z18248; MUID:98365468
A;Accession: T14867
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1738 <RIV>
A;Cross-references: EMBL:AF057019; NID:g3549260; PID:g3549261; PIDN:AAC34582.1
A;Genetics:
A;Gene: abpD
A;Introns: 173/2; 1680/1

Query Match   14.6%;   Score 157;   DB 2;   Length 1738;
Best Local Similarity 26.7%;   Pred. No. 0.24;
Matches   56; Conservative   39; Mismatches   85; Indels   30; Gaps   7;

Qy   20 DAEFLKNELDSVKAQLSQKDREKRDSQAIIDTLRDTLEERNATVESLQNALNKAEMLCST 79
         |||:||::||:::::||::|| :||: : ::|||:|||||::|::|::|:||||:| |
Db 1296 DLNQLKQENQEKEKQLSEKEDEKLQSIQQDLNQLNDDQIRKN---EKLK---EKEEQL--- 1346

Qy   80 LKKQMKFLEQRQDETKQAREEAHRLKCKMKTMEQ----IEILLQSQRSEVEEMIRDMGVG 135
         ||||:|:: :| |:|::| :: | |: ||| :|:||:|:|:|||:|::|:::
Db 1347 LKLQQDFNDQQSQOQLKQLEEKLSEKENQLQOLKQENEINQLNQQQOSNEIIQQLKDQLLK 1406

Qy 136 QSAVEQLAVYCVSLKKEYENLKEARKATGELADRLKK------------DLVSSRSKLKTLNTEL 188
         |||:|:|: ::|:|::||:|:| :|: ::| ::||| :|:|||:||:|||:|
Db 1407 QQQQEQ---------------QENNNEKEIERLIQEI-EQLKQQOEIDQSELSNKEIKIQTTQQEF 1456

Qy 189 DQAKLELRSAQKDLQSADQEITSLRKKSDD 218
         | :|::|||:| ::|::|:|| | ||||
Db 1457 DQLSHNRSKDQLHLQQLQOELDQLKQSFPD 1486

RESULT 29
B43402
myosin heavy chain-B, neuronal - chicken
myosin heavy chain-B, neuronal ATPase (EC 3.6.1.32)
N;Contains: myosin ATPase (EC 3.6.1.32)
C;Species: Gallus gallus (chicken)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Jan-2001
A;Accession: B43402; A43402
R;Takahashi, M.; Kawamoto, S.; Adelstein, R.S.
J;Biol. Chem. 267, 17864-17871, 1992
A;Title: Evidence for inserted sequences in the head region of nonmuscle myosin specifi
yosin.
A;Reference number: A43402; MUID:92388144
A;Accession: A43402
A;Molecule type: mRNA
A;Residues: 1-2007 <TAK>
A;Cross-references: GB:M93676; NID:g212448; PIDN:AAA48988.1; PID:g212452
A;Note: the sequence of residues 212-221 and 632-652 and the corresponding nucleotide se
A;Accession: A43402
A;Molecule type: mRNA
A;Residues: 1-211,222-631,653-2007 <TA2>
A;Cross-references: GB:M93676; NID:g212448; PIDN:AAA48985.1; PID:g212449
A;Note: sequence extracted from NCBI backbone (NCBIN:112864)
C;Comment: Alternatively spliced segments 1 and 2 are found exclusively in nonmuscle myd

---

C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Keywords: actin binding; alternative splicing; ATP; coiled coil; hydrolase; methyla
F;1-2007/Product: myosin heavy chain-B, neuronal #status predicted <MYN>
F;1-211,222-631,653-2007/Product: myosin heavy chain-B, nonmuscle #status predicted <
F;88-802/Domain: myosin motor domain homology <MMOT>
F;178-185/Region: nucleotide-binding motif A (P-loop)
F;212-221/Region: alternatively spliced segment 1 #status experimental
F;559-593/Region: alternatively spliced segment 2 #status predicted
F;632-652/Region: alternatively spliced segment 2 #status experimental
F;692-714/Region: actin binding #status predicted
F;875-2007/Domain: coiled coil #status predicted <COI>
F;875-1315/Region:
F;1316-2007/Region: light meromyosin
F;1129/Modified site: N6,N6,N6-trimethyllysine (Lys) #status predicted
F;184/Binding site: ATP (Lys) #status predicted
F;732,742/Active site: Cys #status predicted
F;733,742/Region: S2
F;195/Binding site: phosphate (Thr) (covalent) #status predicted
F;1987/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match   14.6%;   Score 157;   DB 1;   Length 2007;
Best Local Similarity 21.3%;   Pred. No. 0.28;
Matches   65; Conservative   58; Mismatches   92; Indels   90; Gaps   10;

Qy   4 INKLFPDLAQEEENV------------------------LDAEF--LKNELDSVKAQLSQK 38
         :::||| ::|| | ||::| :|::||:|:|||:||
Db 1109 IEELKIQLAKKEEELQAALARGDEEAVQKNNALKVIRELQAQIAELQEDLESEKASRNKA 1168

Qy   39 DREKRDSQAIIDTLRDTLEERNATVESLQNALNKAEMLCSTLKK------------QMKFL 87
         :::||| :|::|:|||||||::|::| :||:|:|::|| |:   ::|||
Db 1169 EKQKRDLSEELEALKTELEDTLDTTAAQELRTKREQVEAELRLKAIEEETKNHEAQIQEI 1228

Qy   88 EQRQ----DETKQAREEAHRLK------------CKMKTMEQIELLLQSQR--- 122
         ||| |::|::|::|||:| |||||:|:|||:|:|:|
Db 1229 RQRHATALEELSEQLQOSAVEQLAVYCVSLKKEYENKNKQGLESDNKELACEVKVLQQVKAESEHRKKL 1288

Qy 123 -SEVEEMIRDMGVGQGSAVEQLAVYCVSLKKEYEN----LKEARKA------- 162
          :|:|:||| | :||:|:|:|::| ::|:|::|| |:|:|
Db 1289 DAQVQELTAKVTEGERLRVELAEKANKLQNELDNVSSLLEEAEBKKGIKFAKDAASLESQL 1348

Qy 163 --TGELADRLKKDLVSSRSKLKTLNTE----LDQAKLELRSAQKDLQ----SADQEITSLR 213
          :||:|:|||:|::|||:||:|||:| |::|::|||:| ::| ::|::|| |
Db 1349 QDTQELLQEETRQKLNLSSRIQLEEEKNNLQEQEEEEARKNLEKQMLALQAQLAEAK 1408

Qy 214 KKSDD 218
        ||||
Db 1409 KKVDD 1413

RESULT 30
A27224
myosin heavy chain II - Acanthamoeba castellanii
myosin heavy chain II - Acanthamoeba castellanii myosin ATPase (EC 3.6.1.32)
N;Contains: myosin ATPase (EC 3.6.1.32)
C;Species: Acanthamoeba castellanii
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Jan-2001
A;Accession: A27224
R;Hammer III, J.A.; Bowers, B.; Paterson, B.M.; Korn, E.D.
J;Cell Biol. 105, 913-925, 1987
A;Title: Complete nucleotide sequence and deduced polypeptide sequence of a nonmuscle
A;Reference number: A27224; MUID:87308395
A;Accession: A27224
A;Molecule type: DNA
A;Residues: 1-1509 <HAM>
A;Cross-references: GB:Y00624; GB:M12702; GB:M12703; GB:M19549; NID:g5585; PIDN:CAA68
A;Genetics:
A;Introns: 69/3; 119/3; 181/2
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Keywords: actin binding; ATP; coiled coil; hydrolase; methylated amino acid; nucleo
F;92-775/Domain: myosin motor domain homology <MMOT>
F;182-189/Region: nucleotide-binding motif A (P-loop)
F;544-576/Region: actin binding #status predicted
F;660-682/Region: actin binding #status predicted
F;848-1227/Domain: coiled coil #status predicted <COI>

F;1228-1247/Domain: hinge <HIN>
F;1248-1482/Domain: coiled coil #status predicted <CO2>
F;1483-1509/Domain: carboxyl-terminal <CBT>
F;133/Modified site: N6,N6,N6-trimethyllysine (Lys) #status predicted
F;188/Binding site: ATP (Lys) #status predicted

Query Match   14.6%;   Score 156.5;   DB 1;   Length 1509;
Best Local Similarity   20.9%;   Pred. No. 0.22;
Matches   59;   Conservative   59;   Mismatches   91;   Indels   73;   Gaps   7;

```
Qy    10 DLAQEENVLD-------------------------------AEFLKNELDSV----------
            ::  ::     :                                :::  :::  ::
Db  1017 DALADAENISETLRSKLKNTERGADDVRNELDDVTATKLQLEKTKKSLEEELAQTRAQLE 1076

Qy       ------------------------------KAQLS 36
Db  1017                                            1076

Qy    37 QKDREKRDSQAIIDTLRDTLEENRATVESLQNALNKAEMLCSTLKKQMKFLEQRQDETKQ 96
            ::::                   :::::  ::  ::  ::::   :::
Db  1077 EEKSCKEAASSKAKQLGQQLEDARSEVDSLKSKLSAAEKSLKTAKDQNRDLDEQLEDERT 1136

Qy    97 AR-----EEAHRLRCKMKTMEQIELLLQSQ------RSEVEEMIRDMGVGQ----- 136
            ::       ::     ::                 :: ::  :::
Db  1137 VRANVDKQKKALEAKLTELEDQVTALDGQKNAAAAQAKILKTQVDETKRRLEEAASAAR 1196

Qy   137 -----SAVEQLAYYCVSLKKEYENLKEARKATGELADRLKKDLV-----SSRSKLKT 183
              :::             ::   ::           ::         :::
Db  1197 LEKERKNALDEVAQLTADLDAERDSGAQQRRKLNTRISELQSELENAPKTGGASSEEVKR 1256

Qy   184 LNTELDQAKLELRSAQ-----------KDLQSADQEITSLRKKSDD 218
           ::::                      :::::::  :::::::
Db  1257 LEGELERLEEELLTAQEARAAAAEKNLDKANLELELRQEADD 1298
```

RESULT 31
S07537

myosin heavy chain, smooth muscle, splice form 2 - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jul-2000
C;Accession: S07537; S10449
R;Babij, P.; Periasamy, M.
J. Mol. Biol. 210, 673-679, 1989
A;Title: Myosin heavy chain isoform diversity in smooth muscle is produced by differenti[al]
A;Reference number: S07537; MUID:90139920
A;Accession: S07537
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-412 <BAB>
A;Cross-references: EMBL:X16261
R;Babuj, P.; Periasamy, M.
submitted to the EMBL Data Library, August 1989
A;Reference number: S10449
A;Accession: S10449
A;Molecule type: mRNA
A;Residues: 134-412 <BA2>
A;Cross-references: EMBL:X16261; NID:g56648; PIDN:CAA34347.1; PID:g56649
A;Experimental source: Sprague-Dawley; smooth muscle; clone RAMHC15
A;Comment: For an alternate splice form see (PIR:S10450).
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Keywords: alternative splicing; ATP; cardiac muscle; heart; muscle

Query Match   14.5%;   Score 156;   DB 2;   Length 412;
Best Local Similarity   21.4%;   Pred. No. 0.062;
Matches   54;   Conservative   55;   Mismatches   95;   Indels   48;   Gaps   7;

```
Qy    10 DLAQEENVLDAEFLKNELDSVKAQLSQK-----------------DREKRDSQAIIDTLRDTLEE 58
            ::                                         :::::
Db   162 ELMLQEDLAAAERARKQADLEKEELASSLSGRNTLQDEKRRLEARIAQLEEELEE 221

Qy    59 RNATVESLQNALNKAEMLCSTLKKQMFLEQRQDETKQAREEAHR------------- 103
            :::                  :::          :::
Db   222 EQGNMEAMSDRVRKATLQAEQLSNELVTERSAAQKNESARQQLERQNKELRSKLQEVEGA 281
```

Qy   104 LKCKMK-TMEQIELLLQSQRSEVEEMIRDMGVGQSAVEQLAYYCVSLKKEYENLKEARKA 162
Db   282 VKAKLKSTVAALEAKIVQLEEQIEQEAREK---QAATKLLKQKDKKLKEVLLQVEDERK- 337

Qy   163 TGELADRLKKDLVSSRSKLKTNTELEDQQAKLE-------LRSAQKDLQSADQ------E 208
Db   338 ---MVEQYKEQAEKGNTKVKQLKRQLEEAEEESQRINANRRKLQRELEDEATESNEAMGRE 394

Qy   209 ITSLRKKSDDPP 220
Db   395 VNALKSKLRGPP 406

RESULT 32
S60943

RUD3 protein - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein O5028; protein YOR216c; protein YOR50-6
C;Species: Saccharomyces cerevisiae
C;Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 21-Jul-2000
C;Accession: S60943; S67109; S71718
R;Galisson, F.; Dujon, B.
Yeast 12, 877-885, 1996
A;Title: Sequence and analysis of a 33 kb fragment from the right arm of chromosome X
A;Reference number: S60943; S67109; S71718
A;Accession: S60943
A;Description: Sequence and analysis of a 33 kb fragment from the right arm of chromo[some]
A;Reference number: S60938
A;Accession: S60943
A;Molecule type: DNA
A;Residues: 1-484 <GAL>
A;Cross-references: EMBL:X92441; NID:g1050762; PID:g1050768
R;Boyer, J.; Fairhead, C.; Gaillon, L.; Galisson, F.; Michaux, G.; Thierry, A.; Dujon
submitted to the Protein Sequence Database, July 1996
A;Reference number: S67109
A;Accession: S67109
A;Molecule type: DNA
A;Residues: 1-484 <BOY>
A;Cross-references: EMBL:Z75124; NID:g1420502; PID:e252397; PID:g1420503; MIPS:YOR216
A;Experimental source: strain S288C
R;Galisson, F.; Dujon, B.
Yeast 12, 877-885, 1996
A;Title: Sequence and analysis of a 33 kb fragment from the right arm of chromosome X
A;Reference number: S71713; MUID:96437977
A;Accession: S71718
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-484 <GAV>
A;Cross-references: EMBL:X92441; NID:g1050762; PIDN:CAA63179.1; PID:g1050768
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1995
A;Cross-references: SGD:S0005742; MIPS:YOR216c
C;Genetics:
A;Gene: SGD:RUD3
A;Map position: 15R
C;Function:
A;Description: suppressor of uso1-1 transport defect

Query Match   14.4%;   Score 155;   DB 2;   Length 484;
Best Local Similarity   24.3%;   Pred. No. 0.083;
Matches   51;   Conservative   52;   Mismatches   67;   Indels   40;   Gaps   8;

Qy   24 LKNELDSVKAQLSQKDREKRDSQAIIDTLRDTLEEN---ATVESLQNALNKAEMLCSTL 80
Db   96 LREEIERLKLELSHKDQETPNEDFRNELANVIKERDEFKTQYDTLLSKISSMKSIFNKM 155

Qy   81 KKQMKFLEQRQDETKQAREEAHRLRLCKMKTMEQIELLLQSQRSEVEEMIRDMGVGQSAVE 140
Db   156 KEAQKQLEEVQEOLTE--YESQNLKIKKK----------LEATKTENSEL-----QSTI- 197

Qy   141 QLAYYCVSLKKEYENLKEARKATGE----------LADRLKKDLVSSRSK-LKTLNTEL 188
Db   198 -----VTLNTELENLEKEQESTEEVFLEYESRIEALEDE-KHDIIEKHSKELNTYRKEK 250

Qy   189 DQAKLELRSAQKDLQSADQEITSLRKKSDD 218
Db   251 DQLNLQVQELMIILENNKQDISDLRTERDE 280

RESULT 33
B70356
chromosome assembly protein homolog - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 02-Jun-2000
C;Accession: B70356
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov
V.
Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID: 98196666
A;Experimental source: strain VF5
A;Genetics:
A;Gene: xcpC
C;Superfamily: chromosome segregation protein SMC1
A;Accession: B70356
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-1156 <AQF>
A;Cross-references: GB;AE000699; NID:g2983238; PIDN:AAC06839.1; PID:g2983243; GB:AE00065

```
Query Match    14.4%;    Score 155;    DB 2;    Length 1156;
Best Local Similarity    20.9%;    Pred. No. 0.2;
Matches    47;    Conservative    63;    Mismatches    73;    Indels    42;    Gaps    7;

Qy    11  LAQEEENV---LDAEFLKNELDSVKAQLSQKDREKRDSQAIID---TLRDTLEERNATVE   64
Db   207  LKEEKLEKFKELQRIKRETEA-KILLKEKERILNELSLSRESLEDITFQIQ         265

Qy    65  SLQNALNKAEMLCSTLKKQM--------KFLEQRQDETKQAREEAHRLCKKMKTMEQIEL  116
Db   266  ENEKELNERERLLKEVNEKNIMPFKEKYGKFTAEIENAEBSIKEKERELKESENRVKNLEE 325

Qy   117  LLQSQRSEVEEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKATGELADRLKKDLVS 176
Db   326  LINNLLSDKENLEREVGTLQLELEK--------LKEEYKSLKEV----------       361

Qy   177  SRSKLKTLNTELDQAKL---ELRSAQKDLQSADQEITSLRKKSDD               218
Db   362  EREKLRELEEEEERLKITFDEVKKLEEEKEKLTEKLNSLNKEKQE               406
```

Qy   69 ALNKAEMLCSTLKKQMK-FLEQRQDETKQAREEAHRLCKKMKTME-QIELLLQSQRSEVE 126
Db   798 ALEE-------LKKEKETIIKEKQELQLQSKSAESESSALKVVQVOLEQLQQOAAASGE 850

Qy   127 EMIRDMGVGQSAVEQLAVYCVSLKKEYE-------------NLKEARKATGELAD   168
Db   851 EGSKTVAKLHDEISQLKSQAEETQSELKSTESNLEAKSKQLEAANGSLEEEAKKSGQLQE 910

Qy   169 ---RLKKDLVSSRSKLKTLNTELDQAKLELRSAQKDLQSADQEITSLRKKSDD   218
Db   911 QITKLKSEVEETQAALSSYHTDVESKTKQLEAANAALEKVNKEVAESRAEASD   963

RESULT 35
T25454
hypothetical protein B0432.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T25454
A;Molecule type: DNA
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-380 <HEN>
A;Cross-references: EMBL;U80836; PIDN:AAB37891.1; GSPDB:GN000020; CESP:B0432.6
C;Genetics:
A;Experimental source: strain Bristol N2; clone B0432
A;Gene: CESP:B0432.6
A;Map position: 2
A;Introns: 104/3; 190/3; 211/0; 283/3; 304/3; 325/3
R;Henkhaus, J.; Wohldmann, P.
submitted to the EMBL Data Library, December 1996
A;Description: The sequence of C. elegans cosmid B0432.
A;Reference number: Z20038
A;Accession: T25454

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Query Match    14.4%;    Score 154.5;    DB 2;    Length 380;
Best Local Similarity    31.3%;    Pred. No. 0.069;
Matches    67;    Conservative    47;    Mismatches    69;    Indels    31;    Gaps    14;

Qy     2  TIINKLFFDLAQEENVLDAE--FLKN-ELDSVKAQLSQKDREKRDSQAIIDTLRDTLEE   58
Db   176  TILNVNFKKIG-ENENIFKFKICFLKNKKIDFQKLENFPKILTKKPHKIIPESLQNA--E 232

Qy    59  RNATVESLQNALNK--AEMLCSTLKKQMKFLEQRQDETKQAREEAHRLCKKM--KTMEQI 114
Db   233  RN--VHTAQNEISKLNTELAQSVTRIELFLAENR--ELKQEFEE-KVVECEVLKEHIRQI 287

Qy   115  ELLLQSQRSEVEEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKATGELADRLKKDL 174
Db   288  DLELKNKQSDMERALLQI-----SAAEQKAA-----KKELE-LIEAEKHL-----KLYESR 332

Qy   175  VSSRSK-LKTLNTELDQAKLELRSAQKDLQSADQ                           207
Db   333  LSDRERDLNAKNLEIDRLKLDLDAARRNLQKLEQ                           366
```

RESULT 36
T22976
hypothetical protein F59A2.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C;Accession: T22976; T23157
A;Molecule type: DNA
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-1133 <WIL>
A;Cross-references: EMBL;Z34801; PIDN:CAA84332.1; GSPDB:GN000021; CESP:F59A2.6
A;Experimental source: clone F59A2
R;Lightning, J.
R;Burton, J.
submitted to the EMBL Data Library, June 1994
A;Reference number: Z19645
A;Accession: T22976

submitted to the EMBL Data Library, October 1995
A;Reference number: Z19700
A;Accession: T23157
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1133 <W2>
A;Cross-references: EMBL:Z66514; PIDN:CAA91344.1; GSPDB:GN00021; CESP:F59A2.6
A;Experimental source: clone K01A11
C;Genetics:
A;Gene: CESP:F59A2.6
A;Map position: 3
A;Introns: 13/2; 43/3; 107/3; 413/3; 492/3; 567/3; 635/3; 710/3; 738/3; 795/2; 1008/3; 1

Query Match   14.4%;   Score 154.5;   DB 2;   Length 1133;
Best Local Similarity   24.1%;   Pred. No. 0.21;
Matches   57;   Conservative   62;   Mismatches   77;   Indels   41;   Gaps   10;

```
Qy   13 QEEENVLDAE--FLKNELDSVKAQLSQKDREKRDS-QAIIDTLRDTLEE----------RNAT 62
           ||||  |:||  |||||||||||||||||||||| |||||||||||||          ||||
Db   93 EESKKVLESEKQAFENEKEQEREEQLAKAMEKLNSEQNTLDEVTKKLEQSEEEVLAARGA 152

Qy   63 VESLQNALNKAEMLCSTLKKQMKFLEQRQDETKQAREE------------AHRLKCKMKTMEQ 113
Db  153 IQELTELKEESEKTEFSTARTELEAVSKLDSSETSLKEPSDMIEAMKIQLINCEKQKDEA 212

Qy  114 IELLLQSQRSEVEEMIRDMGVGQ----------SAVEQLAVYCVSLKKEYENLKEARKATGE 165
Db  213 VELLKQ-KLEEVERNMSDVEVQKQLLLESTTSEMKQHAEAAEIVKKQ---LEEAQSS--- 265

Qy  166 LADRLKKDLVSSRSKLKTL------NTELDQAKLELRSAQKDLQSADQEITSLRKKSD 217
Db  266 -IENLKDAENERN-LKTALESDESSAISEITKQMEAAKKELEASEKEKSELREQMD 320
```

RESULT 37
C35815
myosin heavy chain 3, muscle - fruit fly (Drosophila melanogaster) (fragment)
C;Species: Drosophila melanogaster
C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 20-Jun-2000
C;Accession: C35815
R;Collier, V.L.; Kronert, W.A.; O'Donnell, P.T.; Edwards, K.A.; Bernstein, S.I.
Genes Dev. 4, 885-895, 1990
A;Title: Alternative myosin hinge regions are utilized in a tissue-specific fashion that
A;Reference number: A35815; MUID:90346288
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1175 <COL>
A;Cross-references: EMBL:X53155; NID:g8219; PIDN:CAA37308.1; PID:g2546936
A;Note: the authors translated the codon TGC for residue 649 as Lys, and AAG for residue
C;Genetics:
A;Gene: FlyBase:Mhc
A;Cross-references: FlyBase:FBgn0002741
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Keywords: ATP

Query Match   14.4%;   Score 154.5;   DB 2;   Length 1175;
Best Local Similarity   22.8%;   Pred. No. 0.22;
Matches   59;   Conservative   56;   Mismatches   91;   Indels   53;   Gaps   9;

```
Qy   10 DLAQEEENVLD--AEFLKNELDSVKAQLSQKDREKRDSQAIIDTLRDTLEERNATVESLQ 67
Db  903 DDAREQLGISERRANALQNELEESRTLLEQADRGRRQAEQELADAHEQLNEVSAQNASIS 962

Qy   68 NALNKAEMLCSTLKKQMKFL----EQRQDETKQAREEAHRLKCKMKTMEQIELLLQSQRS 123
Db  963 AAKRKLESELQTLHSDLDELLNEAKNSEEKAKKAMVDAARLADELRAEQDHAQTOEKLRK 1022

Qy  124 EVEEMIRDMGV----------GQSAVEQLAVYCVSLKKEYE------------NLKEAR 160
Db 1023 ALEQQIKELQVRLDEAEANALKGGKKAIQKLEQRVRELENELDGEQRRHADAQKNLRKSE 1082

Qy  161 KATGELA-----DRLK----KDLVSS-RSKLKTLNTELDQAK--------LELRSAQKDLQ 203
Db 1083 RRVKELSFQSEEDRKNHERMQDLVDKLQOKIKTYKRQIEEAEEIAALNLAKFRKAQOELE 1142

Qy  204 S------ADQEITSLRKK 215
Db 1143 EAEERADLAEQAISKFRAK 1161
```

RESULT 38
D35815
myosin heavy chain 4, muscle - fruit fly (Drosophila melanogaster) (fragment)
C;Species: Drosophila melanogaster
C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 13-Feb-1998
C;Accession: D35815
R;Collier, V.L.; Kronert, W.A.; O'Donnell, P.T.; Edwards, K.A.; Bernstein, S.I.
Genes Dev. 4, 885-895, 1990
A;Title: Alternative myosin hinge regions are utilized in a tissue-specific fashion t
A;Reference number: A35815; MUID:90346288
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1175 <COL>
A;Cross-references: EMBL:X53155
C;Genetics:
A;Gene: FlyBase:Mhc
A;Cross-references: FlyBase:FBgn0002741
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Keywords: ATP

Query Match   14.4%;   Score 154.5;   DB 2;   Length 1175;
Best Local Similarity   22.8%;   Pred. No. 0.22;
Matches   59;   Conservative   56;   Mismatches   91;   Indels   53;   Gaps   9;

```
Qy   10 DLAQEEENVLD--AEFLKNELDSVKAQLSQKDREKRDSQAIIDTLRDTLEERNATVESLQ 67
Db  903 DDAREQLGISERRANALQNELEESRTLLEQADRGRRQAEQELADAHEQLNEVSAQNASIS 962

Qy   68 NALNKAEMLCSTLKKQMKFL----EQRQDETKQAREEAHRLKCKMKTMEQIELLLQSQRS 123
Db  963 AAKRKLESELQTLHSDLDELLNEAKNSEEKAKKAMVDAARLADELRAEQDHAQTOEKLRK 1022

Qy  124 EVEEMIRDMGV----------GQSAVEQLAVYCVSLKKEYE------------NLKEAR 160
Db 1023 ALEQQIKELQVRLDEAEANALKGGKKAIQKLEQRVRELENELDGEQRRHADAQKNLRKSE 1082

Qy  161 KATGELA-----DRLK----KDLVSS-RSKLKTLNTELDQAK--------LELRSAQKDLQ 203
Db 1083 RRVKELSFQSEEDRKNHERMQDLVDKLQOKIKTYKRQIEEAEEIAALNLAKFRKAQOELE 1142

Qy  204 S------ADQEITSLRKK 215
Db 1143 EAEERADLAEQAISKFRAK 1161
```

RESULT 39
A35815
myosin heavy chain 1, muscle - fruit fly (Drosophila melanogaster) (fragment)
C;Species: Drosophila melanogaster
C;Date: 12-Oct-1990 #sequence_revision 28-Mar-1991 #text_change 20-Jun-2000
C;Accession: A35815
R;Collier, V.L.; Kronert, W.A.; O'Donnell, P.T.; Edwards, K.A.; Bernstein, S.I.
Genes Dev. 4, 885-895, 1990
A;Title: Alternative myosin hinge regions are utilized in a tissue-specific fashion
A;Reference number: A35815; MUID:90346288
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1201 <COL>
A;Cross-references: EMBL:X53155; NID:g8219; PIDN:CAA37310.1; PID:g2546938

```
A;Note: the authors translated the codon TGC for residue 649 as Lys, and AAG for residue
C;Genetics:
A;Gene: FlyBase:Mhc
A;Cross-references: FlyBase:FBgn0002741
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Keywords: ATP

Query Match          14.4%;   Score 154.5;  DB 2;   Length 1201;
Best Local Similarity   22.8%;  Pred. No. 0.22;
Matches   59;   Conservative   56;  Mismatches   91;   Indels   53;  Gaps   9;

Qy     10  DLAQEENVLD--AEFLKNELDSVKAQLSQKDREKRDSQAIIDTLRDTLEERNATVESLQ   67
               | :|:| :||||:|| ||: |:|| ::||| | | :::| :| ||||: |:
Db    903  DDAREQLGISERRANALQNELEESRTLLEQADRGRQAEQELADAHEQLNEVSAQNASIS  962

Qy     68  NALNKAEMLCSTLKKQMKFL-----EQRQDETKQAREEAHRLCKCMKTMEQIELLLQSQRS  123
               | | :|: : |::|||||:|     ||:|||:||:||:||:|||::  | ::|:||:  |
Db    963  AAKRLESELQTLHSDLDELLNEAKNSEEKAKKAMVDAARLADELRAEQDHAQTQEKLRK  1022

Qy    124  EVEEMIRDMGV--------------GQSAVEQLAVYCVSLKKEYE-------------NLKEAR  160
               :|:| :| |              | :||:| :|:| ||||               ||| |
Db   1023  ALEQQIKELQVRLDEAEANALKGGKKAIQKLEQRVRELENELDGEQRRHADAQKNLRKSE  1082

Qy    161  KATGELA----DRLK---KDLVSS-RSKLKTLNTELDQAK-----LELRSAQKDLQ  203
               || ||     |||:   |||:|: |||:|| ||||||     |:|:| | ||
Db   1083  RRVKELSFQSEEDRKNHERMQDLVDKLQQKIKTYKRQIEEAEETAALNLAKFRKAQQELE  1142

Qy    204  S--------ADQEITSLRKK  215
               :|: | | :  | |
Db   1143  EAEERADLAEQAISKFRAK  1161
```

```
RESULT   40
B35815
myosin heavy chain 2, muscle - fruit fly (Drosophila melanogaster) (fragment)
C;Species: Drosophila melanogaster
C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 20-Jun-2000
C;Accession: B35815
R;Collier, V.L.; Kronert, W.A.; O'Donnell, P.T.; Edwards, K.A.; Bernstein, S.I.
Genes Dev. 4, 885-895, 1990
A;Title: Alternative myosin hinge regions are utilized in a tissue-specific fashion that
A;Reference number: A35815; MUID:9034628B
A;Accession: B35815
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1201 <COL>
A;Cross-references: EMBL:X53155; NID:g8219; PIDN:CAA37311.1; PID:g2546939
A;Note: the authors translated the codon TGC for residue 649 as Lys, and AAG for residue
C;Genetics:
A;Gene: FlyBase:Mhc
A;Cross-references: FlyBase:FBgn0002741
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Keywords: ATP

Query Match          14.4%;   Score 154.5;  DB 2;   Length 1201;
Best Local Similarity   22.8%;  Pred. No. 0.22;
Matches   59;   Conservative   56;  Mismatches   91;   Indels   53;  Gaps   9;

Qy     10  DLAQEENVLD--AEFLKNELDSVKAQLSQKDREKRDSQAIIDTLRDTLEERNATVESLQ   67
               | :|:| :||||:|| ||: |:|| ::||| | | :::| :| ||||: |:
Db    903  DDAREQLGISERRANALQNELEESRTLLEQADRGRQAEQELADAHEQLNEVSAQNASIS  962

Qy     68  NALNKAEMLCSTLKKQMKFL-----EQRQDETKQAREEAHRLCKCMKTMEQIELLLQSQRS  123
               | | :|: : |::|||||:|     ||:|||:||:||:||:|||::  | ::|:||:  |
Db    963  AAKRLESELQTLHSDLDELLNEAKNSEEKAKKAMVDAARLADELRAEQDHAQTQEKLRK  1022

Qy    124  EVEEMIRDMGV--------------GQSAVEQLAVYCVSLKKEYE-------------NLKEAR  160
               :|:| :| |              | :||:| :|:| ||||               ||| |
Db   1023  ALEQQIKELQVRLDEAEANALKGGKKAIQKLEQRVRELENELDGEQRRHADAQKNLRKSE  1082

Qy    161  KATGELA----DRLK---KDLVSS-RSKLKTLNTELDQAK-----LELRSAQKDLQ  203
```

```
Db   1083  RRVKELSFQSEEDRKNHERMQDLVDKLQQKIKTYKRQIEEAEETAALNLAKFRKAQQELE  1142
               || ||     |||:   |||:|: |||:|| ||||||     |:|:| | ||
Qy    204  S--------ADQEITSLRKK  215
               :|: | | :  | |
Db   1143  EAEERADLAEQAISKFRAK  1161
```